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Database Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Sequence: Run on: OM nucleic - nucleic search, using sw model Minimum DB Maximum DB Total number of hits satisfying chosen parameters: Searched: Scoring table: Perfect score: Title: seq length: 0
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Pred. ŏ. is the number of results predicted by chance to have a

REFERENCE AUTHORS TITLE

SOURCE ORGANISM

DEFINITION ACCESSION VERSION KEYWORDS

RESULT 1 VCH6514 LOCUS

ALIGNMENTS

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.

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Characterisation of the lot/thva locus from Vibrio cholerae Characterisation of the lot/thva locus from Vibrio cholerae	Vibrio cholerae Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales; Vibrionaceae; Vibrio.	AJ006514.1 GI:3201563 AJ006514.1 GI:3201563 lgt gene; prolipoprotein diacylglyceryl transferase; thyA; thymidylate synthetase. Vibrio cholerae	VCH6514 2909 bp DNA linear BCT 05-JUN-1998 Vibrio cholerae lgt and thyA genes.	

1141 GGATGACATGGGACGCGTGTATGGTGTTCAGGGTAGAGCTTGGGCTAAGCCTGATGGTGG		6
	GAGAAGGTTTGTTATGCCTCAGGGTTATCTGCAGTTTCCCAATATTGACCCCGTATTGTT 60	Qy 1 Db 1
	/ Match 100.0%; Score 2909; DB 1; Length 2909; Local Similarity 100.0%; Pred. No. 0; Local Similarity 100.0%; Pred. No. 0; Indels 0; Gaps 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0; C	Query Match Best Local Matches 290
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μр	Carlin,N.I.A. Qy Direct Submission Submitted (29-MAY-1998) Carlin N.I.A., Department of Molecular Biology, SBL Vaccin AB, FMB, Jv 30, Stockholm, S-105 21, SWEDEN	
	9)	JOURNAL U

>—> H-	ACTGTACCTGAAGCAATACCGTGTAGTGGGCCTCGGCCAATTGCATTTTGTAGAA	•
222	101 GCCCACGAGAGGAACCATTAGGCTGGTTGTGGTCGATGAAGATTGAACTAATACCGT 161 CACTGTACCTGAAGCAATACCGTGTAGTGGGCCTCGGCCAATCGCATTTTGTAGAAT	
CAGA 2100 CAGA 2100	GTGCCAATGTTCGCACCTAAGGTAAATGGGTAGATTTCACGCACTTTCAGCACGC 	
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\GG 1920 \GG 1920	1861 CTTACAAGCCCAAGTTGAGATGAGCTCAGCACCTTTAATAGGCAGTTCGCGTAAGAAAGG	
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CC: 1740 		
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GT 1620 	1561 AGCGCCTCAGTTCCATATCAATCCAAAGATTAAAACACTGCAGGATTTGGAAACTTGGGT	
CC 1560	O1 CATTTACCAAGAT	
3CA 1500 3CA 1500	ATGGCA ATGGCA	
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CAT 1320 CAT 1320	1261 TGAAATTCTTAACTTCTACAATCCGGGTGAATTTCACATGGGGTGTTTGCGCCCTTGCAT	
)GAGG 1260 GAGG 1260	1201 TCATATTGACCAGTTGAAAAAGATTGTTGATGATGATTGAGCCGTGGCGTTGATGACCGA	

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ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                   REFERENCE
AUTHORS
TITLE
                                                                                                                                           FEATURES
Query Match 100.0%; Score 2909; Best Local Similarity 100.0%; Pred. No. 0; Matches 2909; Conservative 0; Mismatches
                                                                                                                                                                        JOURNAL
                                                                                                                           source
                                                                                                                                                                                                                                            Vibrio cholerae
Vibrio cholerae
Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
Vibrionaceae; Vibrio.
                                                                                                                        Carlin,N. and Lebens,M.R.

Method of producing thy a<->strains of vibrio cholerae, such strains and their use Patent: WO 9961634-A 1 02-DEC-1999;
CARLIN NILS (SE); SBL VACCIN AB (SE); LEBENS MICHAEL R (SE)
Location/Qualifiers
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      0;
      Gaps
      0;
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2161 CACTGTACCTGAAGCAATACCGTGTAGTGGGCCTCGGCCAATCGCATTTTGTAGAATTTC 2220	.081 CTGGGATGCTAATGCCAATTTAAACCAAGCATGGCTCAACAATCCTTACCGTAAAGGTGA 114	. `
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1501 11CAGICLARICCCURIIIAACSCOOTHICH	601 TGGTAAACCTCGTCCGCTAGGCAGCGTATCCGGACTGTTTTTAGCTGGATACGGTACATT 660	
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120 ISANAII IAAU ICIACAAI ICUSSISANII ICUSSISISII ISUSSISII ISUSSISII ISUSSISII ITUSSISII ILIII	181 AGTCTCTGACTTGTTATTCGCCGGCTTTTTAGGTGTAGTGATCGGTGGCCGAGTTGGTTA 240	
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gene="VC0669"	9 (100	TITLE DNA sequence of both chromosomes of the cholera pathogen Vibrio	TIT
YYA" Ommil bmbnt (2043 3035)		Sellers, P., McDonald, L., Utterback, T., Fleishmann, R.D.,	
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/COOKER SCENT CONTROL SCENT CONTROL OF MICH CONTROL OF		3	ORG
			KEYWORDS
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			AE004153
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e, MD 20850, USA 9	FEATURES	2341 AAGCTGGGTTTCAAGCCCTGTGATGACAGGTTTGGTAATCGGTTTGATAAAATCAAAACC 2400	문
Direct Submission Submitted (14-JUN-2000) The Institute for Genomic Research, 9712	TITLE JOURNAL	2341 AAGCTGGGTTTCAAGCCCTGTGATGACAGGTTTGGTAATCGGTTTGATAAAATCAAAACC 2400	ş
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LOBSES I CO 9931, Heidelberg, J. F., Eisen, J.A., Nelson, W.C., Clayton, R.A., Gwinn, M.L., Dodson, R.J., Haft, D.H., Hickey, E.K., Peterson, J.D., Umayam, L.A.,	AUTHORS	2221 ACGTGCGGGCCAACCATCAAACTCTTCATCAGTTTGCCCATCACCGTAATGGCGACGAA 2280 2221 ACGTGCGGGCCAACCATCAACTCTTCATCAGTTTGCCCATCACCGTAATGGCGACGAA 2280	문 5
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LGYTTLSMNTSNVAKVKYLVRHSELAELTQLAEQALTQPYGRETYNMMLAYIEKHGFA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MLRIGICGKINAIKEFTRGLPVIDGDGYRLNVGIVICNNHGQVF
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/notee="similar to PID:882723 GB:U00096 SP:Q46930

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3124. .3705
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AACGGATGTGCCTTGGGCTTTTGTATTCCCTAATGGTGGCCCACTGCCGCGCCATCCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTCGATCGGCCCTCTAGCGGTGCGCTGGTATGGCTTGATGTATTTTGGTGGGTTTTCCTTTT
                                                                                                                                                                           GACTGGCGGTATGTCCTTCCACGGCGGCTTATTGGGTGATCACCGCCATGTTCTGGTA
                                                                                                                                                                                                                                                              GACTGGCGGCATGTCCTTCCACGGCGGCTTATTGGGTGTGATCACCGCCATGTTCTGGTA
                                                                                                                                                                                                                                                                                                                                              AGTCTCTGACTTGTTATTCGCCGGCTTTTTAGGTGTAGTGATCGGTGGCCGAGTTGGTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                   AGTCTCTGACTTGTTATTCGCCGGCTTTTTTAGGTGTAGTGATCGGTGGCCGAGTTGGTTA
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                                                                 ATTCGGTTTGGGGATGGGACGTATCGGTAACTTTATGAATAGTGAACTTTGGGGGACGAGT
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                                                                                                                                                     TGCGCGTAAAAACCAACGCACCTTCTTTGGTGTGGCCGATTTTTGTTGCCCCCTTGGTGCC
                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="mrqyldlcqrivdogwwenertgkrcltvinadltydvgnnqr
Plyttrksfwrkavaellgy ingydnadfrqufkrtwdananingaminbyrkged
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similarity; putative"
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Pred. No. 0;
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9294 ATCGTGGATGGTGGCACTGGCGAAAGCACGGGAAACTCTTCTTACAGCGCATATGGCC 2581 AAGGCTGACGAGAGTATTGGTCACAGTAGTACCAATATTTGGCACCCATCACCATAGGAAT	Q Q Q Q B	8214 GATGGCACAGATCACAGGAAAAAGCCCGGGCTTGGCGTATCACAAAACGTCGACATGCGCA 8273 1501 CATTTACCAAGATCAACTCGAATTGATGCGCGATGTGCAGCTAAAACGTGAGCCATTCCC 1560
	Q, B Q	381 ATGTGATGTGCCCTTGGGGTTGAATTTCAACATGGTGCAGGTTTATGTGTTCCTTGCGCT
1—1 1—1	dg VQ	8034 TGAAATTCTTAACTTCTACAATCCGGGTGAATTTCACATGGGGTGTTTGCGCCCTTGCAT 8093 1321 GTACAGCCATCATTTTCATTGCTGGGGGATACCTTGTATCTCAACAGTACTCAGCGTTC 1380
2341 AAGCTTGGTTTCAAGACCTGTTATGACAGGTTTGGTAATCGGTTTGATAAAGTCAAAACC	D Q D &	1201 TCATATTGACCAGTTGAAAAAGATTGTTGATGATTGAGCCGTGGCGTTGATGACCGAGG 1260
21 ACC	р ф У	141 GGATGACATGGGACGCGTGTATGGTGTTCAGGGTAGAGCTTGGGCTAAGCCTGATGGTGG
2161 CACTGTACCTGAAGCAATACCGTGTAGTGGGCCTCGGCCAATCGCATTTTGTAGAATTTC	B &	//94 GCICGGCIATATICGIGGITACGAIAAIGCGGGAITTICGCCAATITAGGTACCAAAAC /853 1081 CTGGGATGCTAATGCCAATTTAAACCAAGCATGGCTCAACAATCCTTACCGTAAAGGTGA 1140
2101 GCCCACGAGAGGAACCATTAGGCTGGTTGTGGTCGATGAAGATTGAACTAATACCGTAAC	Qу	734 CAATCAGTTICCTCTAGTCACTACACGCAAGAGTTTTTTGGAAAAGCCGCCGTGGCCGAGTT 021 GCTCGGCTATATTCGTGGTTACGATAATGCGGCGGATTTTCGCCAATTAGGTACCAAAAC
2041 AGTGCCAATGTTCGCACCTAAGGTAAATGGGTAGATTTCACGCACTTTCAGCACGCCAGA	D Q	4 ACGAACGGGCAAGCGTTGTTTGACTGTGATTAATGCCGATTTGACCTACGATGTGGGCAA 1 CAATCAGTTTCCTCTAGTGACTACACGCAAGAGTTTTTTGGAAAGCTGCCGTAGCCGAGTT
1981 CAGAGCAAACACGGCAAACTCACCAGAGAGAGCGGTTGCGGCGAGCAGAGCAGTAATACA	Qy db	CROACAGLATITIAGATCITIGICAGCGCATCGTCGATCAAGGTGTTTGGGTTGAAAAAIGA ACGAACGGGCAAGCGTTGTTTGACTGGACTTAATGCCGATTTGACCTACGATGTGGGCAA
1921 AATACCGTAAATCAAGACCGTAGCCATCAAGTTAAAGCTTAAGTGCACCAGCGCAATTTG	Qу	1 GAAACAGTATTTAGATCTTTTTGTCAGGGCATCGTGGATCAAGGTGTTTGGGTTGAAAATGA
1861 CTTACAAGCCCAAGTTGAGATGAGCTCAGCACCTTTAATAGGCAGTTCGCGTAAGAAAGG	Q	TIGGICITACAAGCGCGGTITGIATCAAGACCGIGTAGCAGCAAAATAGGGTAGTIAGGI
1801 AATGCTGCCGGGGATGACGACAAACACCCCAATAAGTAACTCACCACCACCACTTTTGCT	g dy	AATGGGGCAAATCCTCTCCTTACCTATGGTGATCATCGGTATTTTGATGATGATGATGATGATGATGATGATGATCATCGGTATTTTGATGATGATGGT
1741 CGAAGGTCGGGAGCTTTTTTATACAGATGATGCTTTAACGCTTAAGCGGTAGGGCAAG	p Q	661 CCGCTTCCTTGTGGAATACGTCCGTGAGCCAGATGCTCAGTTGGGTCTGTTTGGTGGCTT 720
11-1	Db Oy	601 TGGTAAACCTCGTCCGCTAGGCAGCGTATCCCGACTGTTTTTAGCTGGATACGGTACATT 660
$\delta = \delta$	D Q	ACAGCTTTATGAATTCGCCTTAGAAGGCGTGGTTCTGTTCTTTATTCTTAATTGGTTTAT
		7254 AACGGATGTGCCTTGGGCTTTGTATTCCCTAATGGTGGCCCACTGCCGGCCATCCTTC 7313

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Oy 551 GAATTCGCCTTAGAAGGCGTGGTTCTGTTCTTTATTGGTTATTGGTATACCT	Query Match 47.8%; Score 1390.8; DB 1; Length 1410; Best Local Similarity 99.1%; Pred. No. 0; Matches 1398; Conservative 0; Mismatches 12; Indels 0; Gaps	ORIGIN	MYSHHFSLIGDTLYLNSTQRSCOVPLGLINGKINVOVYVELALMAGITGKKEGIAHKIV NAHIYQDQLELMRDVQLKREPFPAPQFHINPKIKTLQDLETWVTLDDFDVTGYQFHDP IQYPFSV"	/translation="mrqyldlcqrivdqqwwvenertgkrchtvinadltypdvgnnop PLVTTRKSFWKAAVAELLGYIRGYDNAADFROLGTKTWDANANLNQAWLNnpyrkScbD	/db_xref="G41:3114981" /db_xref="G801SS-PROT:066108" /db_xref="S801SS-PROT:066108"	/ranni_rable=rl. /product="khymidilate synthase" /protein_id="CAA76645.1"		/db xref="taxon:666" gene 2891140 /gene="thy0"	NA"	01000	JOURNAL Direct Submitsion JOURNAL Submitted (16-APR-1998) J.A. Benitez, Centro Nacional de Investigaciones, Cientificas, PO Box 6990, La Habana, CUBA	828	20490577		<pre>Valle,E., Ledon,T., Cedre,E., Campos,J., Valmaseda,T., Rodriguez,B., Garcia,L., Marrero,K., Benitez,J., Rodriguez,S. Fando,R.</pre>	Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionates; Vibrionaceae; Vibrio. REFERENCE 1	W. h	SON	VCTHYAG LOCUS VCTHYAG VCTHYAG 1410 bp DNA linear BCT 01-NOV-2000 DEFINITION Vibrio cholerae thyA gene.	4004	2881 TTTCGTGGTCAGCGAAATCGGCGCTGCAG	9594	Qy 2821 CATCGCGACTGCAAGAAGTAGTAAATACAGCATGAAAGCCAAGTTTGCCCAACGTAGGCC	Db 9534 AGCAAATTCAAATAGAACTTTGCCTTGATCGCCGGTTGCCCATTTAAAACCGCTGCCGAC	2761	Th 9474 TGACATATTCACTTCACTTCACTTCACTTCACTTCACTT
1081 GATTTGACGTCACCGGATATCAGTTCCACGATCCTATTCAGTATACCCGTTTTCAGTCTAA 1	GATTTTGACGTCACGGATATCAGTTCCAGGATCCTATTCAATACCGGTTTTCAGTCTAA	1571	PHILIP OY 1511 GATCAACTCGAATTGATGCGGGATGTGCAGCTTAAAACGTGAGCCATTCCCAGCGCCTCAG 1570	g da		13	Qy 1331 CATTITICATIGCTGGGGGATACCTIGTATCTCAACAGTACTCAGCGTTCATGTGATGTG	721 AACTTCTACAATCCGGGTGAATTTCACATGGGGTGTTTGCGCCCTTGCATGTACAGCCAT	71 AACTTCTACAATCCGGGTGAATTTCACATGGGGTGTTTGCGCCCTTGCATGTACAGCCAT	Qy 1211 CAGTTQAAAAAGTTQTTGATTQAGCCGTGGCGTTGATGACCGAGGTGAAATTCTT 1270	01 GACGCGTGTATGGAGTTCAGGGTAGAGCTTAGGCTAAGCCTGATGGTGGTCATATTGAC	Qy 1151 GGACGCGTGTATGGTGTTCAGGGTAGAGCTTAGGCTTAAGCCTGATGGTGGTCATATTGAC 1210	541 AATGCCAATTTAAACCAAGCATGGCTCAACAATCCTTACCGTAAAGGTGAGGATGACATG	Db 481 ATTCGTGGTTACGATAATGCGGCGGATTTTCGCCAATTAGGTACCAAAAGGTGAGGATGACT 540 Ov 1091 AATGCCAATTTAAAACCAAGCATGGCTCAACAATCCTTACCGTAAAGGTGAGGATGACATG 1150	1031 ATTCGTGGTTACGATAATGCGGCGGATTTTCGCCAATTAGGTACCAAAACCTGGGATGCT	Db 421 CCTCTAGTCACTACACGCAAGAGTTTTTGGAAAGCCGCCGTGGCCGAGTTGCTCGGCTAT 480	361 AAGUGTTIGITTIGACTIGIGATTAATIGUUGATTITAAUGUTAUGATIGUTGACGATAUGATIGUTGACGATAGATTIGACTITAGACATAGATTITAGACTITAGACATAGATAGATAGATAGATAGATAGATAGATAGATA	وب ر	OY 851 TTAGATCTTTGTCAGCGCATCGTCGATCAAGGTGTTTGGGTTGAAAATGAACGAAC	Db 241 AAGCGCGGTTTGTATCAAGACCGTGTAGCAGCAAAATAGGGTAGTTAGGTGAGACAGTAT 300		731 GGGCAAATCCTCTCTCTTACCTATGGTGATCATCGGTATTTTGATGATGGTTTTGGTCTTAC	2880 Db 121 GTGGAATACGTCCGTGAGCCAGATGCTCAGTTGGGGCTGTTTGGTGTCATTTCAATG 180	Oy 671 GTGGAATACGTCCGTGAGCCAGATGCTCAGTTGGGTCTGTTTGGTGGCTTCAATG	Db 61 CGTCCGCTAAGCCAGACTGTTTTTAGCTGGATACCGGTACAGTTCCTTC	9533 OV 611 CGTCCGCTAGGCAGCGTATCCGGACTGTTTTTAGCTGGATACGGTACATTCCGCTTCCTT 670

1988 AACACGGCAAACTCACCAGAGACACGGGTTGCGGCGAGCAGAGAGAG		1868 GCCCAAGTTGAGATGAGCTCAGCACCTTTAATAGGCAGTTCGCGTAAGAAAGGAATACCG 1927	1808 CCGGGGATGACGACAAACACACCCAATAAGTAACTCACCACCACCATTTTGCTCTTACAA 1867 	1748 CGGGAGCTTTTTTTATACAGATGATGCTTTAACGCTTAAGCGGTTAGGGCAAGAATGCTG 1807	ATTCAGGCGGTATGGCTTGATGGGTTTTATATATAAAAAAGCTCCCGAAGGT 17 	Query Match 42.0%; Score 1222; DB 6; Length 1222; Best Local Similarity 100.0%; Pred. No. 0; Matches 1222; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		JOURNAL PAtent: WO 9961634-A 3 02-DEC-1999; CARLIN NILS (SE); SBL VACCIN AB (SE); LEBENS MICHAEL R (SE) FEATURES Location/Qualifiers source 1 1222	REFERENCE 1 AUTHORS Carlin, N. and Lebens, M.R. TITLE Method of producing thy a<->strains of vibrio cholerae, such strains and their use	_	N Sequence 3 from Patent W099616 V AX009483 AX009483.1 GI:9996768	AX009483	1931 ATCAAGACCGTAGCCATCAAGTTAAAGCTT 1960 	1871 CAAGTTGAGATGAGCTCAGCACCTTTAATAGGCAGTTCGCGTAAGAAAGGAATACCGTAA 1930 	1811 GGGATGACGACAAACACCCAATAAGTAACTCACCACCATTTTGCTCTTACAAGCC 1870 	1751. GAGCTTTTTTTATACAGATGATGCTTTAACGCTTAAGCGGTTAGGGCAAGAATGCTGCCG 1810	1141 TCCCGTATTCAGGCGGTATGGCTTGATGGGTTTTACATAGGAAAAGCTCCCGAAGGTCGG 1200
SOURCE	ACCESSION VERSION KEYWORDS	RESULT 6 AY143429 LOCUS DEFINITION	Db Qy	P &	Qy da	Qy Db	Db Oy	. Qу	рb	D 29	Qγ	B &	QY	Db Qy	D 29	Db Qq	da
Vibrio cholerae NISM Vibrio cholerae Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;	ION AY143429 N AY143429 1 GI:23343945 DS		2888 GTCAGCGAAATCGGCGCTGCAG 2909 	2828 ACTGCAAGAAGTAGTAAATACAGCATGAAAGCCAAGTTTGCCCAAAGGTAGGCCTTTCGTG 2887	TCAAATAGAACTTTGGCTTGATCGCCGGTTGCCCATTTAAAACCGCTGCCGACCATCGCG	2708 TGAATCAGTGCCGTTGCCACTAAACCAATCATCAATCCTGCAATTGGGTGGG	2648 TCAACCGGTAACCCACCGGCAACGAGACCAACAATAATAGAAGTCACCGTGCTTGAGGAT 2707 	2588 ACGAGAGTATTGGTCACAGTACCAATATTGGCACCCATCACCATAGGAATCGCGGTT 2647	2528 ATGGTGCCACTGGCGAAAGCACGCGAAACTCTTCTTTACAGCGCATATGGCCAAGGCTG 2587	CCAAACATCATTTCTAGAGGTAGGAAGATCAGCACCGCGAGAAGATTGAAAAAATCGTGG	2408 CTCATATCGCCAGTCGCAAGCAGAGCGAGACGAGCCAGTGTGAGACTTTCTCTAAAATG 2467 	2348 GTTTCAAGCCCTGTGATGACAGGTTTGGTAATCGGTTTGATAAAATCAAAACCTTTCATG 2407 	2288 GCAATACCCAATACGATAAGTGCGACACCACCGAAAGTATTACCCAATACCGAAAGCTGG 2347 	2228 CGGCCAACCATCAAACTCTTCATCAGCTTTGCCCATCACCGTAATGGCGACGAAAATGGTC 2287 	2168 CCTGAAGCAATACCGTGTAGTGGGCCTCGGCCAATCGCATTTTGTAGAATTTCACGTGCG 2227	2108 AGAGGAACCATTAGGCTGGTTGTGGTCGATGAAGATTGAACTAATACCGTAACCACTGTA 2167 	361 ATGTTCGCACCTAAGGTAAATGGGTAGATTTCACGCACTTTCAGCACGCCCAGAGCCCACG 420

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TAAAGGTGAGGATGACATGGGACGCGTGTATGGTGTTCAGGGTAGAGCTTGGGCTAAGCC
                                                                  TACCAAAACCTGGGATGCTAATGCCAATTTAAACCAAGCATGGCTCAACAATCCTTACCG
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Submitted (17-SEP-1998) Carlin N.I.A.,
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Carlin, N.I.A.
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Vibrionaceae; Vibrio.
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      /organism="Vibrio cholerae"
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Query Match
Best Local Similarity
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VAITVMGKLMKSLMVGRAREILQNAIGRGPLHGIASGTVTVTVLVQSSTTTSLMVPLV
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373. .376
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A filamentous phage associated with recent pandemic parahaemolyticus O3:K6 strains
J. Clin. Microbiol. 38 (6), 2156-2161 (2000)
Makino,K., Oshima,K., Kurokawa,K., Yokoyama,K. Tagomori,K., Iijima,Y., Najima,M., Nakano,M., Kubota,Y., Kimura,S., Yasunaga,T., Honda,T., S Hattori,M. and Iida,T. Genome sequence of Vibrio parahaemolyticus: a distinct from that of V cholerae Lancet 361 (9359), 743-749 (2003)
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AP005074.1 GI:28805287
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Vibrio parahaemolyticus
Bacteria; Proteobacteria;
Vibrionaceae; Vibrio.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCCTGCAATTGGGTGGGAAGCAAATTCAAATAGAACTTTGGCTTGATCGCCGGTTGCCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AATAGAAGTCACCGTGCTTGAGGATTGAATCAGTGCCGTTGCCACTAAACCAATCATCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACCCATCACCATAGGAATCGCGGTTTCAACCGGTAACCCACCGGCAACGAGACCAACAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTTACAGCGCATATGGCCAAGGCTGACGAGAGTATTGGTCACAGTAGTACCAATATTGGC
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                                                                                                                                                                                                                                                                                                                       Gammaproteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                       bp DNA chromosome
                                                                        Yokoyama, K., Uda, T.,
Nakano, M., Yamashita, A.,
Honda, T., Shinagawa, H.,
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complete

sequence, BCT 05-MAR-2003

2909 405

> 452 2862

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692 2622 752 2562

812 2502 872 2442

2382 992 2322

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Park, K.S.,

Vibrionales,

pathogenic mechanism

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Information Research Center; 3-1, Yamadaoka, Suita, Osaka 565-0871, Japan (E-mail:ken@gen-info.osaka-u.ac.jp, URL:http://www.gen-info.osaka-u.ac.jp/, Tel:81-6-6879-8365,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oshima, K., Kurokawa, K., Makino, K., Yokoyama, K., Yasunaga, T., Honda, T., Shinagawa, H., Hattori, M. and Iida, T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gastroenteritis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct
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LNKLEVIPELNEANVRLHYDSGIRYHFGPVEITGSQUENRVESMRPFEIGEPYLVSD
VGEYNQNLSNTDWFSSYFVEPDLSKLEDGRELPIKVSLAPAAKNQIETGIGYSTDTGV
RGTLKWKKPWVSARGHSFNTALSLSKPEQTITAGYKIPLDDVLREYYQLQFGLKHLDN
RDTESLESNLAVERHWLTDGGWHKTTYVRHLYENFSQGLQDGVGVLFGATFSRTTRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ILLGMGCFWGAERLFWQLDGVVSTSVGYAGGFTPNPTYEEVCTGKTGHTEVVRVVVFDE
RVISLAQLLAVFWEKHDPTQGMRQGNDLGTQYRSAIYTYSQDQQEIADKSKLQYQQAL
EAELRSTITTEIVPAGPYYFAETYHQQYLAKNPDGYCGIGGTGVCFPPSLQG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement (399. .1037)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="VP0306"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="MLREFAVYRPLQVARFVKTLFKGQFFIVGVGSFCFDNGKVLLPD
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TEBFEKLSÞSLRFFÁGGDNNIRGYGYESISÞVDESGALTGÁKYILSSTLEYQYRVYGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="VP0307"
1205. .2917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /evidence=not_experimental
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  WWAATFYDIGDAFNDTPEWKSGAGVGIRWASPVGPVSFDFAWGLDEKPNNEFRIHFSL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'gene="VP0307"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  dentity 74 in 208 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  evidence=not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          fnote="similar to PIR:S56442 percent identity 49 in 63 aa"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'gene="VP0305"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  translation="MLNKQTLISIEDALPGREQPMQIEDCHFVNQSSLTAPLAHHQQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="similar to GB:AAF95690.1 (AE004324) percent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'gene="VP0305"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     chromosome="1"
                                                                                                                                                                                                                                                                                                                                                                                                                                   codon start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .298900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             _strain="RIMD 2210633"
_xref="taxon:670"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               experimental
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LKTQLPFDVSIKNVQAQWPLFQQSDYQVVSVPSLAKGSLLGYBYALETKASGKDIRAV
DVALNGKGTLEQIDLESLVVETLGGELSGKVARMAREINWQADLIKNIQPGLOWKE
AEGDISGSLSTSGSITEQGGWQVSLPKLDIDGILRGYPLNVEGQLEASDKNGKGEDIQ
LTTQGLALSHGPNQLSAKGKLDKQILMDVENVEPDFAKSVPDLAGKMQGKVALRGSIK
EPDINLDLALNQINWQQQANVETITIKLGDVFVNFPDFAKSVPDLAGKMQGKVALRGSIK
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LEVSGDSKLHQLTLDVVSDLVSTSLEIEGTFKQKPEMIWDGALRRLTLSSQQGPWSLQ
KSTRAVKVNIDKQIANVQAHCWLQAKSSVYCLTEBISVGKTGAKLAINDENFDQIKQFL
PPETKLQGSVNAQAFAKWAPEKKPEVTISDISVAKFGQVEQALEQPIKVGWDSFSFKAAL
AKDKLDAEWLFDVKUNGDLSGKVSLLAVSSEKFTIDGKVALSTFHILDFLAFLIGBYSL
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GIITPDGKLLEITGDADWRDLGGVSDTVILNKDLOPVDEVAAMPFNVETDINIKI
GDDFQLAAFGLKGGLKGSLAVTQKDKOGFIVGEVNIVDEVDAVAMFRYGGQDEJATGULKGLKGGLKGSLAVTQKDKOGFIVGEVNIVDEVSRSFGQDLATEGKTLINN
GDDFQLAAFGLKGGLKGSLAVTQKDKOGFIVGEVNIVDEVSRSFGQDLATEGKTLINN
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2914..6681
/gene="VP0308"
                                                                                                                                                                                                                                                          /tx=ns1ation="mrvliigammmllsacAqttlpastsvtdwqafgkqsaldglre
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ffqhdydagrmssagapi"
                                                                                                                                                                     complement (7607. .8137)
                                                                                                                                                                                                                    complement (7607. .8137)
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                                                                                  note="similar to GB:AAF95686.1 (AE004323) percent dentity 90 in 176 aa"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene="VP0310"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="similar to GB:AAF95687.1 (AE004323) percent dentity 64 in 115 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'gene="VP0309"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   transl_table=1:
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                                                           codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="similar to GB:AAF95688.1 (AE004323) percent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             codon_start=1
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GPADQPYVSIKAIRNPDNTQDDVIAGVRVTGPASDPSVEIFSEPAMPQANALSYLLRG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EKALPQLKVENIQGSLFPRFALQNVSFVDBSLHIDAKVERIALAINFRCFFDPKVCVD
ELALQGVNCQWEELPPASEEPBEETPPLRSISTPPIAFVNKYSFNDINVVLGNQID
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IPLTVEARRLDIHNFKLAGETPVIVNHLGIVARAGGBRVDVKTLELDMPEVEGKLSTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              translation="MIKKMFKWTKWLSLSLIGLLLLITIFVATVLFTHPGLKLAIWGA
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Best Local Sim
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/gene="VP0312"
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AAGLGDITGAVGTENV(GEAQOKLDVXANDKFKAALEARDQVCGVASEEEDEAVAFNK
ELNQNAKYVLMDFLDGSSNIDVNSVGTIFJYRRVSFIGTPATEEDFLQPGHKQF
ELNQNAKYVLVYTTGGGVNGFTYDSIGSFCLSHENMMIPEDGKIYSINEGNYIRF
PQGVKKYIKYCQENVPEDGRPYTSRYIGSLVADFHRNLLKGGIYLYPSTQSHPQGKLR
PQGVKKYIKYCQENVPEDGRPYTSRYIGSLVADFHRNLLKGGIYLYPSTQSHPQGKLR
LYECNPMAFLIEQAGGIASDGVNRIMDIKPTELHQRVPFFVGSKNMVRKVEEFLELH
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/protein_id="BAC58574.1"
/protein_id="BAC58574.1"
/db_xref="G1:28805294"
/translation="MSLNHVPAGKSLPEDIYVVIEIPANADPIKYEVDKDSGAVFVDR
/translation="MSLNHVPAGKSLPEDIYVVIEIPANADPIKYEVDKDSGAVFVDR
/fransParkTion="MSLNHVPAGKSLPEDIYVVIEIPANADPIKYEVDKDSGAVFVDR
/franspryckyrogyNNTLSLDGDPVDVLVPTPYPLMFGSVIRCRPVGVLKMTDESGE
DAKVVAVPHSKISKEYEHIQDVGDIPELLKAQITHFFERYKELESGKWVKVDGWADVE
AAKAEILQSYERAQNK"
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/transl.table=11
/product="fructose-1,6-bisphosphatase"
/protein_id="BAC58575.1"
/db_xref="GI:28805295"
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/gene="VP0313"
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/gene="VP0313"
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dentity 88 in 336 aa"
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Submitted (13-DEC-2002) Genotech Corp., Yuseong-gu, Daejeon 305-811, South Korea
3 (bases 1 to 301442)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complete sequence. AE016798 AE016798
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (13-DEC-2002) Department of Microbiology, Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rhee, J.H., Kim, S.Y., Chung, S.S., Lee, S.E. and Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Jeong, H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antigens Preferentially Expressed in Septicemic Patients Infect. Immun. 71 (10), 5461-5471 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Characterization and Pathogenic Significance of Vibrio vulnificus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and
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Kim, Y.R., Lee, S.E., Kim, C.M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vibrio vulnificus CMCP6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chung, S.S.,
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complement (1070
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                                                                                                                                                                                                                                                                                                   /locus_tag="VV10312"
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1
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Kwang-Ju 501-746,
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South Korea
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2452. .3348
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2201. .2443
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omplement(soco
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protein_id="AAO08843.1"
db_xref="GI:27359905"
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transl_table=
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215.437 ÓRÉTRIGATIVACIONA PROCESSA PRODUCTIVA PROPRANCISCA 215378 218 TICTRONATTURA CUSTUCCINGUA CONCUENTA NUTRA TRANSCANCISCA 215378 215.317 TICTRANACTURA CUSTUCCINGUA CONCUENTA NUTRA TRANSCANCISCA 215378 308 GOANGUACHA CUSTUCTURA CUSTUCTURA TRANSCANTINA CUSTUA ANA CONCUENTIVA CUSTUA CONCUENTIVA CUSTUA CUSTUA CONCUENTIVA CUSTUA CUSTUA CONCUENTIVA CUSTUA	Qy 128 Db 215497 Qy 188

JOURNAL Submitted (29-MAY-2002) Shih Feng Tsai, National Health Research Institutes, Division of Molecular and Genomic Medicine; 128, Yen-Chiu-Yuan Road, Sec 2, Taipei, Taiwan 115, Republic of China (E-mail:petsai@nhri.org.tw, Tel:886-2-8146-1041, Fax:886-2-2789-0484) COMMENT This sequence was determined by the Sequencing Core of the National Yang-Ming University Genome Research Center (YMGC; http://genome.ym.edu.tw). FEATURES 1249150 /organism="Vibrio vulnificus YJ016" /organism="Vibrio vulnificus YJ016" /strain="YJ016" /db_xref="taxon:196600" /chromosome="I"	Bacteria; Proteobacteria; Gammaproteobacteria; Vibrional Vibrionaceae; Vibrio. 1 Chen,C.Y., Wu,K.M., Chang,Y.C., Chang,C.H., Tsai,H.C., I Liu,Y.M., Chen,H.J., Shen,A.B., Li,J.C., Su,T.L., Shao,C Lee,C.T., Hor,L.I. and Tsai,S.F. Comparative Genome Analysis of Vibrio vulnificus, a Mari Genome Res. 13, 2577-2587 (2003) 2 (bases 1 to 249150) Chen,C.Y., Wu,K.M. and Tsai,S.F. Direct Submission	LOCUS AP005332 AP005332 DEFINITION Vibrio vulnificus YJ016 DNA, chromosome I, complete genome, section 3/14. ACCESSION AP005332 BA000037 VERSION AP005332.1 GI:37197435 KEYMORDS SOURCE Vibrio vulnificus YJ016 ORGANISM Vibrio vulnificus YJ016	Qy 1688 TAA 1690 Db 213937 TAA 213935 RESULT 10	QY 1568 CAGTTCCATATCAAACAATTAAAACACTGCAGGATTTTGGAAACTTTTGGTCACTTTTG 1627	QY 1448 CAGATCACAGGGAAAAAGCCGGGCTTTGGCGTATCACAAGATCGTCAATTGCCGCACATTTAC 1507	Db 214417 GACCAATTGCGTAAAATTGTCGATGACCGCGCGGAGTAGACGATCGCGGGAGATC 214358 Qy 1268 CTTAACTTCTACAATCCGGGGGGAATTTCACATGGGGTTTTGCGCCTTGCATGTACAGC 1327	QY 1208 GACCAGTTGAAAAAGATTGTTGATGATTAGAGCCGTGGGGTTGATGACCGAGGTGAAATT 1267
gene CDS	gene CDS	CDS	gene	CDS	gene repeat_region gene	CDS	gene
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68 GGCCCTCTAGCGGTGCGCTATGGCTTGATGTATTTGGTGGGTTTCCTTTTTGCTATG
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/product="conserved hypothetical protein"
/protein_id="BAC93285.1"
/protein_id="BAC93285.1"
/db_xref="GI:37197446"
/translation="MSNKTSIEGLSALLHTLMLIPQHRWITVRELQQQLALLDIHRTT
/translation="MSNKTSIEGLSALLHTLMLIPQHRWITVRELQQQLALLDIHRTT
RSIKRYLDDIIVDVFNVECDSMSMPHVYRKTSEQLLKLNKQEMALLATDQQVLTTAGS
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/gene="VV0522"
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EPLGLSVQCDALLLLFRLSGQHTIRTLALPLIDEASVSTFSFTYPTDFNVERFMREHA
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Pred. No. 1.7e-249;
0; Mismatches 6;
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Query Ma Best Loo Matches Qy Db Db Db Db	REFERENCE AUTHORS TITLE JOURNAL FEATURES SOURCE ORIGIN	RESULT 12 AX009482 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM	8 8 8 8	8 8 8	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2
y Match Local Similarity 100.0%; Pred. No. 1.9e-248; Local Similarity 100.0%; Pred. No. 1.9e-248; Local Similarity 100.0%; Pred. No. 1.9e-248; Bagaaagerrative 0; Mismatches 0; Indels 0; Gaps 0; 1 GAGAAGERRATGECTCAGGGTTATTCTGCAGTTTCCCAATATTGACCCCGTATTGTT 60	Carlin, N. and Lebens, M.R. Method of producing thy acceptations and their use Patent: WO 9961634-A 2 02-D) CARLIN NILS (SE); SBL VACCII Location/Qualifier 1. 838 /organism="Vibrio of mol type="unassig" /db_xref="taxon:66"	3 4	1620 TCACTTTGGATGATTTTGACGTCACCGGATATCAGTTCCACGATCCTATTCAATACCCGT 1679	ACATTTACCAAGATCAACTCGAATTGATGCGCGATGTGCAGCTAAAACGTGAGCCATTCC CAGCGCCTCAGTTCCATATCAATCCAAAGATTAAAACACTGCAGGATTTGGAAACTTGGG	1320 TGTACAGCCATCATTTTCATTGCTGGGGATACCTTGTATCTCAACAGTACTCAGCGTT 1379
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l (bases 1 to 10719) May,B.J., Zhang,Q., Li,L., Paustian,M.L., Whittam Kapur,V. Complete genomic sequence of Pasteurella multocida, Proc. Natl. Acad. Sci. U.S.A. 98 (6), 3460-3465 (20 21145866 21248100 2 (bases 1 to 10719) 3 (bases 1 to 10719) 4 (birect submission Submi	AE006043 10719 bp DNA lin Pasteurella multocida PM70 section 10 of 204 o genome. AE006043 AE004439 AE006043.1 GI:12720282 Pasteurella multocida Pasteurella multocida Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellaceae; Pasteurella.	661 CCGCTTCCTTGTGGAATACGTCCGTGAGCCAGATGCTCAGTTGGGTCTGTTTGGTGGCTT	541 ACAGCTTTATGAATTCGCCTTAGAAGGCGTGGTTCTGTTCTTATTCGTTTATTGGTTTAT		

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Pred. No. 5.2e-241;
0; Mismatches 507;
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                                          Moreno,J.A., Bosch,M., Badiola,I., Llagostera,M.
Direct Submission 1998) Departmento De Genetica
Submitted (12-MAY-1998) Departmento De Genetica
(Unidad De Microbiologia), Universidad Autonoma
Edificio Cn, Bellaterra, Barcelona 08193, Spain
Location/Qualifiers
                                                                                                                                                            Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellaceae; Pasteurella.
                                                                                                                                                                                        Pasteurella multocida
Pasteurella multocida
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 /organism="Pasteurella
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Best Local Similarity

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gene 705. 1811 /gene="HI0900"	/ COUGH B-CELLE 1 // CTAINS Table=11 // CTAINS Table=11 // product="dihydrofolate reductase (fola)" // product="dihydrofolate reductase (fola)" // protein id="AAC2259:1" // protein id="AAC2259:1" // Ab xref="GI:1573919" // LTAINS1ation="MTFSLIVATTLNNVIGKDNQMPWHLPADLAWFRQNTTGKPVIMG // CTAINS1ation="MTFSLIVATTLNNVIGKDNQMPWHLPADLAWFRQNTTGKPVIMG // CTAINS1ation="MTFSLIVATTLNNVIGKDNQMPWHLPADLAWFRQNTTGKPVIMG // CTAINS1ation="MTFSLIVATTLNNVIGKDNQMPWHLPADLAWFRQNTTGKPVIMG // CTAINS1ation="MTFSLIVATTLNNVIGKDNQMPWHLPADLAWFRQNTTGKPVIMG" // CTAINS1ation="MTFSLIVATTGKPVIMG" // CTAINS1ation="MTFSLIVATTGKPVIMG" // CTAINS1ation="MTFSLIVATTGKPVIMG" // CTAINS1ation="	CDS complement (122604) /gene="H10899" /note="shinlar to GB:D10483 SP:P00379 GB:J01609 GB:V00276 GB:X05108 percent identity: 53.16; identified by sequence similarity; putative"	J. 11345 /organism="Haemophilus influenzae Rd KW20" /mol_type="genomic DNA" /db xref="taxon:71421" gene complement(122604) /gene="H10899"	Direct Submission Submitted (28-MAY-1998) Medical Center Dr. Rock The whole genome was sh On Sep 30, 1996 this se Location/Quali	incorporated their annotation into the /notes fields of the corresponding H. influenzae genes REFERENCE 5 (bases 1 to 11545) AUTHORS White,O., Clayton,R.A., Kerlavage,A.R., Fleischmann,R.D., Peterson,J., Hickey,E., Dodson,R. and Gwinn,M.	Medical Center Dr. Rockville, MD 20850, USA The H. influenzae sequence has been updated by R. Fleischmann. New database matches have been assigned, product names have been improved, and a number of frame shifts have been corrected. We gratefully acknowledge the work of Tatusov et. al. We have	Medical Center Dr, Rockville, MD 20850, USA 4 (bases 1 to 11545) White,O., Clayton,R.A., Kerlavage,A.R. and Fleischmann,R.D. Direct Submission Submitted (27-SEP-1997) The Institute for Genomic Research,	996) vage,A.R. an	MEDLINE 95350630 PUBMED 7542800 REFERENCE 2 (bases 1 to 11545) AUTHORS Tatusov,R.L., Mushegian,A.R., Bork,P., Brown,N.P., Hayes,W.S., Borodovsky,M., Rudd,K.E. and Koomin,E.V. TITLE Metabolism and evolution of Haemophilus influenzae deduced from a whole-genome comparison with Escherichia coli		Pasteurellaceae; Haemophilus. REFERENCE 1 (bases 1 to 11545) AUTHORS Fleischmann, R.D., Adams, M.D., White, O., Clayton, R.A., Kirkness, E.F., Kerlavage, A.R., Bult, C.J., Tomb, J., Dougherty, B.A., Merrick, J.M., McKenney, K., Sutton, G.G., FitzHugh, W., Fields, C.A.,
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	29	GGTTATGTGATCTTCTACAATTTTGATCTGTTGCTGACCCTCTTTATTTA	TGGCGGACGTGTT 3512	AAGTCTCTGACTTGTTATTCGCCGGCTTTTTAGGTGATGGGTGATCGGTGGCCGAGTT 235	TGCTATGTTGGCCAATCGCCGAGCGGATCGCGCGGGCAGTGGTTGGACGCGT 175	TCGATCGGCCCTCTAGCGGTGCGCTGGTATGGCTTGATGTATGGTGGGTTTC 115	AGAAGGTITGTTATGCCTCAGGGTTATCTGCAGTTTCCCAATATTGACCCCGTAITGTTT 61	25.6%; Score 744.2; DB 1; Length 11545; ilarity 66.7%; Pred. No. 4.9e-219; Conservative 0; Mismatches 538; Indels 27; Gaps 4; Qy	/ Jene="http://www.ss856197	DNSIFIETĀNAIVRQGILFRQTELLKLIQEEFPQVTGFEITINP	/transl_table=11 Qy /product="H. influenzae predicted coding region HI0907" /protein_id="AAC22569.1" Db /db_xref="GI:1573930" DV /db_xref="GI:1573930" Ov	cal protein; identified by GeneMark;	15815)	/db_xref="GI:1573925" Qy /translation="MDAAKVRSEFDEKMMRYALELADKAEALGEIPVGAVLVDDARNI V IGEGWNLSIVQSDTAHAEIIALRNGAKNIQNYRLLNSTLYVTLEPCTMCAGAILHSR Db IKRLVFGASDYKTGAIGSRFHFFDDYKMNHTLEVTSGVLAEECSQKLSTFFQKRREEK Db IKRLVKSLSDK" Ov	t=1 le=11 onserved hypo ="AAC22565.1"	/gene="HI0906" Qy /note="similar to SP:P30134 PID:296183 PID:987637 PID:1033148 GB:U00096 percent identity: 57.41; identified Db by sequence similarity; putative"			PLITTRESYWKAAIAEFIGYIRGYDNAADFRAIGTKTWDANANKIANWHARGVD DMGRVYGVOGRAWRKPNGETIDQLRKINNITKGIDDRGEILTFRNEGEFDLGCLRPC MITHTESLVGDTLHLTSYQRSCDVPLGLMENQIQVFTFLALMAQITGKKAGKAYHKIV NAHIYEDQLELMRDVQLKRBPFPLPKLEINPDIKTLEDLETWVTMDDFKVVGYQSHEP	/product="thymidylate synthetase (thyA)" /protein_id="AAC22564.1" /db_xref="GI:1573924" /translation="MKQYLELCRRIVSEGEWVANERTGKHCLTVINADLEYDVANNQF	
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		Aaa75484 DNA encod	Ach03831 Human cDN	Aak94823 Human ful	Aak51764 Human pol	Aav59498 Human sod	Adb80585 Ovarian c	Aak52748 Human pol	Aba09555 Human Na-	Abt42286 Toxicity	Adb53745 Primary r	Adb58991 Toxicity-	Aas88385 DNA encod	Adb52673 Primary r	Adb58174 Toxicity-	Abt41887 Toxicity	Abn26172 Human ORF	Aaf28548 Genomic f	Abn26154 Human ORF	Aaf61079 P. putida	Aaz53290 Neisseria	Abz40310 N. gonorr	Continuation (5 of

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RESULT 1
AAZ40646
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 The invention provides a method for producing a Vibrio cholerae thyAnegative strain which is DeltathyA strain lacking thyA gene functions. The method comprises site-directed mutagenesis of the V. cholerae chromosome to delete and/or insert nucleotides at the thyA locus; The V. cholerae thyA-negative strains are used: for overproduction of recombinant proteins; and in vaccines to prevent or treat cholera (or other diseases if engineered to express the appropriate proteins). The thyA gene is also useful for insertion of foreign genes, in a selective and site-specific manner, and the proteins expressed by the thyA gene or by its 5' flanking region, are useful in research and as targets for
                                                                                                                                                                                       Claim
                                                                                                                                                                                                                  New Vibrio cholerae strain defective in the thyA vaccines and for recombinant protein production.
                                                                                                                                                                                                                                                                                 WPI; 2000-062719/05.
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P X P X P X P X P X P X S X X X
                                                                                                       Vibrio cholerae; thyA-negative strain; DeltathyA; thyA gene; cholera; antimicrobial therapy; ss.
                                                                                          Vibrio cholerae
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99WO-EP003509

98SE-00001852

(SBLV-) SBL VACCIN

Carlin N, Lebens MR

New Vibrio cholerae strain defective in the thyA gene, vaccines and for recombinant protein production. for use 'n

Claim 11; Fig 3; 42pp; English

The invention provides a method for producing a Vibrio cholerae thyAnnegative strain which is DeltathyA strain lacking thyA gene functions. The method comprises site-directed mutagenesis of the V. cholerae chromosome to delete and/or insert nucleotides at the thyA locus; The V. cholerae thyA-negative strains are used: for overproduction of recombinant proteins; and in vaccines to prevent or treat cholera (or other diseases if engineered to express the appropriate proteins). The thyA gene is also useful for insertion of foreign genes, in a selective and site-specific manner, and the proteins expressed by the thyA gene or by its 5'-flanking region, are useful in research and as targets for antimicrobial therapy. When used for recombinant protein production, V. cholerae provides high yields with secretion of products into the culture medium for ease of subsequent recovery. The thyA-negative strain can be maintained by thymine complementation, eliminating the need for antibiotic selection. The present sequence represents the nucleotide sequence of the V. cholerae thyA gene 3' flanking region

Sequence 1222 BP; 373 A; 293 C; 289 G; 267 T; 0 U; 0 Other;

100.0%;

42.0%; Score 1222; 100.0%; Pred. No. 0;

DB ω •

Length 1222;

Ś Ş 맑 á á S 밁 문 문 Ś Query Match
Best Local Similarity
Matches 1222; Conserva 2048 1988 1688 1928 1868 1808 241 181 121 61 CGGGAGCTTTTTTATACAGATGATGCTTTAACGCTTAAGCGGTTAGGGCAAGAATGCTG ATGTTCGCACCTAAGGTAAATGGGTAGATTTCACGCACTTTCAGCACGCCAGAGCCCACG CCGGGGATGACGACAAACACACCCAATAAGTAACTCACCACCACCATTTTGCTCTTACAA AACACGGCAAACTCACCAGAGACAGCGGTTGCGGCGAGCAGAGCAGTAATACAAGTGCCA AACACGGCAAACTCACCAGAGACAGAGCGGTTGCGGCGAGCAGAGCAGTAATACAAGTGCCA TAAATCAAGACCGTAGCCATCAAGTTAAAGCTTAAGTGCACCAGCGCAATTTGCAGAGCA TAAATCAAGACCGTAGCCATCAAGTTAAAGCTTAAGTGCACCAGCGCAATTTGCAGAGCA GCCCAAGTTGAGATGAGCTCAGCACCTTTAATAGGCAGTTCGCGTAAGAAAGGAATACCG TAATCCCGTATTCAGGCGGTATGGCTTGATGGGTTTTATATAAAAAAAGCTCCCGAAGGT CCGGGGATGACGACAAACACACCCAATAAGTAACTCACCACCACCATTTTGCTCTTACAA Conservative ۰, Mismatches 0, Indels <u>.</u> Gaps 1867 1987 1807 360 2047 300 1927 180 1747 240 120 60 0

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                                                                                  essential
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                                                  essential gene; cell proliferation
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CACCACCATTTTGCTCTTACAAGCCCAAGTTGAGATGAGCTCAGCACCTTTAATAGG

1030 1902 1090 1842 0

Query Match
Best Local Similarity
Matches 1118; Conserv

Conservative

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Indels

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Gaps

Score 1112.6; Pred. No. 0; 0; Mismatches

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(1) a vector occur imminist proliferation of a ceil. Also included are:
(1) a vector comprising a promoter operably linked to the nucleic acid
(C encoding a polypeptide whose expression is inhibited by the antisense
(C nucleic acid; (2) a host cell containing the vector; (3) an isolated
(C polypeptide or its fragment whose expression is inhibited by the
(C antisense nucleic acid; (4) an antibody capable of specifically binding
(C the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
(C proliferation; (7) identifying a compound that influences the activity of
(C proliferation; (7) identifying a compound that influences the activity of
(C proliferation; (7) identifying a compound that influences the activity of
(C proliferation of the test compound that influences the activity of
(C pathway in which the test compound that influences the activity of
(C pathway in which the test compound that inhibits proliferation of an
(C organism acts; (9) manufacturing an antibiotic; (10) profiling a
(C compound's activity; (11) a culture comprising strains in which the gene
(C product is overexpressed or underexpressed; (12) determining the extent
(C other heach of the strains is present in a culture or collection of
(C strains; or (13) identifying the target of a compound that inhibits the
(C required for proliferation to isolate candidate molecules for rational)
(C arguired for proliferation in cells other than S. aureus, S. typhimurium,
(K. pneumoniae or P. aeruginosa. The present sequence is one of the target
(C prokaryotic essential genes. Note: The sequence data for this patent did
(C electronic format directly from Menance
(C frin, which, which, which is here are an experience data for this patent did
(C electronic format directly from Menance
(C) the province in the printed specification, but was obtained in
06-SEP-2001;
25-OCT-2001;
08-FEB-2002;
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Wall
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:
(1) a vector comprising a promoter operably linked to the nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 14; SEQ ID NO 40937; 1766pp; English.
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                                    ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antisense nucleic acids, useful for identifying proteins or screening homologous nucleic acids required for cellular proliferation to late candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    invention relates to an isolated nucleic acid comprising any one of
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DB; ABU49197.
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Matches 846;
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                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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P-PSDB; AAY26895.
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Ledon Perez TY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wild type; thyA; enzyme; thymidilate synthase; non-toxigenic; mutation; attenuation; immunization; cholera; hemagglutinin protease; biosafety; auxotrophism; replication; vaccine; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Producing strains of Vibrio cholerae with inactivated gene hemagglutinin protease, useful in vaccines against cholera.
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                  GAGGATGACATGGGACGCGTGTATGGTGTTCAGGGTAGAGCTTGGGCTAAGCCTGATGGT
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GAGGATGACATGGGACGCGTGTATGGAGTTCAGGGTAGAGCTTGGGCTAAGCCTGATGGT
                                                         ACCTGGGATGCTAATGCCAATTTAAACCAAGCATGGCTCAACAATCCTTACCGTAAAAGGT
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                                                                            ACCTGGGATGCTAATGCCAATTTAAACCAAGCATGGCTCAACAATCCTTACCGTAAAAGGT
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Valle Diaz E,
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Pred. No. 1.7e-257;
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Silva Cabrera
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AJ, Beni
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New antisense nucleic acids, useful for identifying proteins or screening homologous nucleic acids required for cellular proliferation to late candidate molecules for rational drug discovery programs.

Claim 14; SEQ ID NO 40936; 1766pp; English.

cc encoding a polyophilde whose expression is inhibited by the antisense concleic acid; (2) a host cell containing the vector; (3) an isolated containing the polypeptide or its fragment whose expression is inhibited by the containing the polypeptide; (6) inhibiting cellular containing the polypeptide; (6) inhibiting cellular containing the polypeptide; (6) inhibiting cellular proliferation; (7) identifying a compound that inhibite scellular proliferation; (8) containing a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent contains; or (13) identifying the target of a compound that inhibits the contiferation of an organism. The antisense mucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational continuity of the proliferation in cells other than S. aureus, S. typhimurium, C. K. pneumoniae or P. aeruginosa. The present sequence is one of the target prokaryotic essential genes, Note: The sequence data for this patent did celectronic format directly from WIPO at the printed specification, but was obtained in celectronic format directly from WIPO at the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are: ftp.wipo.int/pub/published_pct_sequences (1) a vector comprising a promoter operably linked to the nucleic acid relates to an isolated nucleic acid comprising any one

Sequence BP; 217 A; 177 C; 216 G; 242 T; 0 U; 0 Other;

Length

Similarity

Ş 밁 Ś 밁 Ś 밁 Ş 망 Ś 밁 밁 Ś 밁 Ś Query Match Best Local Sim Matches 846; 1139 1079 1019 1199 361 301 241 181 959 839 121 999 61 _ AACAATCAGTTTCCTCTAGTGACTACACGCAAGAGTTTTTTGGAAAGCTGCCGTAGCCGAG GAACGAACGGGCAAGCGTTGTTTGACTGTGATTAATGCCGATTTGACCTACGATGTGGGC GTGAGACAGTATTTAGATCTTTGTCAGCGCATCGTCGATCAAGGTGTTTGGGTTGAAAAT GTGAAACAGTATTTAGATCTTTGTCAGCGCATCGTCGATCAAGGTGTTTGGGTTGAAAAT GGTGAAATTCTTAACTTCTACAATCCGGGTGAATTTCACATGGGGTGTTTGCGCCCCTTGC GGTCATATTGACCAGTTGAAAAAGATTGTTGATGATTTGAGCCGTGGCGTTGATGACCGA TTGCTCGGCTATATTCGTGGTTACGATAATGCGGCGGATTTTCGCCCAATTAGGTACCAAA 1078 AACAATCAGTTTCCTCTAGTCACTACACGCAAGAGTTTTTGGAAAGCCGCCGTGGCCGAG GAACGAACGGCCAAGCGTTGTTTGACTGTGATTAATGCCGATTTGACCTACGATGTGGGC GAGGATGACATGGGACGCGTGTATGGAGTTCAGGGTAGAGCTTGGGCTAAGCCTGATGGT GAGGATGACATGGGACGCGTGTATGGTGTTCAGGGTAGAGCTTGGGCTAAGCCTGATGGT ACCTGGGATGCTAATGCCAATTTAAACCAAGCATGGCTCAACAATCCTTACCGTAAAGGT ACCTGGGATGCTAATGCCAATTTAAACCAAGCATGGCTCAACAATCCTTACCGTAAAGGT 1136 Conservative 29.0%; 0; Score 842.4; DB 7; Pred. No. 1.7e-257; 0; Mismatches 6; Indels °, 420 1258 360 1198 240 1018 120 958 60 300 180

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The invention provides a method for producing a Vibrio cholerae thyAnegative strain which is DeltathyA strain lacking thyA gene functions. The method comprises site-directed mutagenesis of the V. cholerae chromosome to delete and/or insert nucleotides at the thyA locus; The cholerae thyA-negative strains are used: for overproduction of recombinant proteins; and in vaccines to prevent or treat cholera (or
                                                                                                                                                   Claim 10;
                                                                                                                                                                                        New Vibrio cholerae strain defective in the thyA vaccines and for recombinant protein production.
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                                                                   TTGGTCTTACAAGCGCGGTTTGTATCAAGACCGTGTAGCAGCAAAATAGGGTAGTTAG
                                                                                                                             CATTTCAATGGGGCAAATCCTCCTCCTTACCTATGGTGATCATCGGTATTTTGATGGT
                                                                                                                                                                                          CCGCTTCCTTGTGGAATACGTCCGTGAGCCAGATGCTCAGTTGGGTCTGTTTGGTGGCTT
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Qy 593 TGGTTTATTGGTAAACCTCGTCCGCTAGGCAGCGTATCCGGACTGTTTTTAGCTGGATAC 652	QY 533 CATCCTTCACAGCTTTATGAATTCGCCTTAGAAGGCGTGGTTCTGTTCTTTATTCTTAAT 592	QY 476 CGAGTAACGGATGTGCCTTGGGCTTTTGTATTCCCTAATGGTGGCCCACTGCCGCGC 532	Qy 416 GTGCCATTCGGTTTGGGGATGGGACGTATCGGTAACTTTATGAATAGTGAACTTTGGGGA 475	QY 356 TGGTATGCGCGTAAAAACCAACGCACCTTCTTTGGTGTGGCCGATTTTGTTGCCCCCTTTA 415	296 GTGTGGACTGGCGCATGTCCTTCCACGGCGGCTTATTGGGTGTGATCACCGCCATGTTC 355	Qy 236 GGTTATGTGATCTTCTACAATTTTGATCTGTTCCTTGCTGACCCTCTTTATTTA	QY 176 GAGCAAGTCTCTGACTTGTTATTCGCCGGCTTTTTAGGTGATCGGTGGCCGAGTT 235	- OY 116 CTTTTTGCTATGTGGTTGGCCAATCGCCGAGCGGATCGCGCGGGCAGTGGTTGGACGCGT 175	62 TCGATCGGCCCTCTAGCGGTGCGCTGGTATGGCTTGATGTATTTGGTGGGTTTC 1	Qy 2 AGAAGGTITGTTATGCCTCAGGGTTATCTGCAGTTTCCCCAATATTGACCCCGTATTGTTT 61		1500001 16 1600001 17 1700001 18 1800001 18	AAT42063 11 1100001 AAT42063 12 1100001 AAT42063 12 1200001 AAT42063 13 1300001 AAT42063 14 1400001	AAT42063 07 700001 AAT42063 08 800001 AAT42063 09 900001 AAT42063 09 900001		Fragment Name Begin End AAT142063_00 1 110000 AAT142063_01 100001 210000	9 9 on (10 of 19) of AAT42063 from base 900001 (Haemophilus influenzae complete 9 solit into 10 fragments 100713 ABC2063 ACC205100 Ast42063
Db 59748 TATCCTTTTCCGTCTAAT 59766	1613 59688 1 <i>6</i> 73	1553 59628	59568	1433 CTTGCGCTGATGGCACAGATCACAGGGAAAAAGCCGGGCTTGGCGTATCACAAGATCGTCGTGTGTTATGGCTATAGATCACGGGCAAAAAAGCCGGGCAAGGCATATCATAAAATTGTG	1373 CAGCGTTCATGTGATGTGCCCTTGGGGTTGAATTTCAACATGGTGCAGGTTTATGTGTTC	Qy 1313 CCTTGCATGTACAGCCATCATTTTTCATTGCTGCGGGATACCTTGTATCTCAACAGTACT 1372	Db 59328 GATAGAGGAGAGTTTTAACCTTGGGGGAATTTGATCTTGGTTGTCTTCGT 59387	1193 GATGGTGGTCATATTGACCAGTTGAAAAAGATTGTTGATGATTTGAGCCGTGGCGTTGAT	OY 1133 AAAGGTGAGGATGACATTGAGGACGCGTGTATTGAGGGTTAAGGCTTTGAGGCTTAGGCCT 1192	OY 1073 ACCAAAACCTGGGATGCTAATGCAATTTAAACCAAGCATGGTCAACAATCCTTACCGT 1132	1013 GCCGAGTTGCTCGGCTATATTCGTGGTTACGATAATGCGGCGGATTTTCGCCAATTAGGT	Oy 953 GTGGGCAACAATCAGTTTCCTCTAGTGACTACACGCAAGAGTTTTTGGAAAGCTGCCGTA 1012	OY 893 GAAAATGAACGAACGGCCAAGCGTTGTTTGACTGGATTAATGCCGATTTGACCTACGAT 952	OY 833 AGTTAGGTGAAACAGTATTTAGATCTTTGTCAGCGCATCGATCAAGGTGTTTGGGTT 892	OY 773 ATGATGGTTTGGTCTTACAAGCGCGGTTTGTATCAAGACCGTGTAGCAGCAAAATAGGGT 832	OY 713 GGTGGCTTCATTTCAATGGGGCAAATCCTCCTTACCTATGGTGATCATCGGTÁTTTTG 772	Qy 653 GGTACATTCCGCTTCTGTGGAATACGTCCGTGAGCCAGATGCTCAGTTGGGTCTGTTT 712 O

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                                                                                                         of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid

(2) encoding a polypeptide whose expression is inhibited by the antisense

(3) an isolated

(4) an antisons is inhibited by the antisense

(5) contisense nucleic acid; (4) an antibody capable of specifically binding

(6) contisense nucleic acid; (4) an antibody capable of specifically binding

(7) identifying a gene polypeptide; (5) inhibiting cellular

(8) proluction the polypeptide; (6) inhibiting cellular

(9) proliferation, (7) identifying a compound that influences the activity of

(1) identifying a gene required for cellular proliferation; (8)

(1) identifying a gene required for cellular proliferation or the biological

(1) pathway in which a proliferation-required gene or its gene product or

(1) manufacturing an antibotic; (10) profiling a

(2) compound's activity; (11) a culture comprising strains in which the gene

(3) product is overexpressed or underexpressed; (12) determining the extent

(4) to which each of the strains is present in a compound that inhibits the

(5) proliferation of an organism. The antisense nucleic acids are useful for

(6) contiferation of an organism. The antisense nucleic acids required

(6) dentifying proteins or screening for homologous nucleic acids required

(6) contiferation in cells other than S. aureus, S. typhimurium,

(7) prokaryotic essential genes on the rhar S. aureus, S. typhimurium,

(8) continued for proliferation in cells other than S. aureus, S. typhimurium,

(8) continued for proliferation in cells other than S. aureus, S. typhimurium,

(9) prokaryotic essential genes of the target for the target for proliferation in cells other than S. aureus, S. typhimurium,

(9) prokaryotic essential genes of the target for the target for proliferation to solate the for the target for proliferation to solate for the target for proliferation to solate for the target for proliferation to solate for the target for the target for t
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06-SEP-2001; 2001US-0094893.

25-OCT-2001; 2001US-0342923P.

08-FEB-2002; 2002US-00072851.

06-MAR-2002; 2002US-0362699P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New antisense nucleic acids, useful for identifying proteins or scrifor homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACA42822
                                                                                                  prokaryotic essential genes. Note:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-MAR-2002; 2002WO-US009107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                e invention relates to an isolated nucleic acid comprising any one of e 6213 antisense sequences given in the specification where expression the nucleic acid inhibits proliferation of a cell. Also included are:
                                                                  form part of the printed specification,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ָס נָי
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Trawick
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Carr G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Haselbeck R, Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            English.
                                                                                                  The sequence
                                                                                    other than S. aureus, S. typhimurium, present sequence is one of the target The sequence data for this patent did teating but the sequence data for this patent did
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene; cell proliferation;
                                                                      but was obtained
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Forsyth
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Xu HH;
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ACA34292 standard; DNA; 852

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ACA34292;

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                              TTTCAGTCTAA 1690
                                                                                           TCACTTTGGATGATTTTGACGTCACCGGATATCAGTTCCACGATCCTATTCAATACCCGT
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Pred. No. 6.8
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emoding a polypeptide whose expression is inhibited by the antisense uncleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense mucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation, (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway or a gene on which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an compound's activity; (11) a culture comprising strains in which the gene product is overskyressed or underexpressed; (12) determining the extent
Query Match
Best Local Similarity
Matches 608; Conserv
                                                                                      to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI;
                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 14;
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06-MAR-2002;
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                                                                             ftp.wipo.int/pub/published
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-OCT-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       e 6213 antisense sequences given in the specification where expression the nucleic acid inhibits proliferation of a cell. Also included are:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antisense nucleic acids, useful for identifying proteins or screening homologous nucleic acids required for cellular proliferation to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 invention relates to an isolated nucleic acid comprising any one
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                                                                                                                                                                                                                                                                                                                                                                                                                                         vector comprising a promoter operably linked to the nucleic acid
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Trawick JD,
 Conservative
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2001US-00948993.
2001US-0342923P.
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2002US-0362699P.
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                                                  246 A; 152 C; 193 G; 261 T; 0 U; 0 Other;
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Carr GJ,
            15.9%;
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           Score 462.2; DB 7;
Pred. No. 4.2e-136;
Mismatches
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                       DB 7;
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Forsyth
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                                                                                                          standard; DNA;
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Antisense; ds; prokaryotic essential gene; cell proliferation;
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                                                                                                                                                                                                  the 513 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid conding a polypeptide whose expression is inhibited by the antisense concerning the vector; (3) an isolated concerning the vector; (3) an isolated concerning the vector; (3) an isolated content whose expression is inhibited by the concerning the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular contining the polypeptide; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway consideration; (7) identifying a compound that influences the activity of confideration of the proliferation, or that inhibits cellular proliferation; (8) cor agene on which the test compound that influences the activity of compound that inhibits ground that influences the activity of compound that inhibits ground that inhibits the gene product is overexpressed or underexpressed; (12) determining the extent compound that inhibits the gene product is overexpressed or underexpressed; (12) determining the extent confideration of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required confideration in cells other than S. aureus, S. typhimurium, confideration for the proliferation, but was obtained in other than S. alternation of the printed specification, but was obtained in
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Matches 570
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25-OCT-2001; 2001US-03429231.
08-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
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Genome; mutagenesis;
detect; growth; anti-
                                                                                                                             Nucleotide sequence of H.influenzae HI0904 gene
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Haemophilus influenzae
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CC Nucleotide sequences AAZ37113-Z37126 are essential Haemophilus influenzae CC genes that have been identified by the methods of the invention. The CC invention relates to a method for locating essential regions of a portion CC of an organism's genome by: (1) in vitro mutagenising DNA having the CC sequence of the region with a transposon; (ii) identifying cells of the CC organism transformed with the mutagenised DNA of (i); and (iii) locating CC the region by detecting the absence of transposons in the region of the CC mutagenised cells containing the mutagenised DNA. The invention also CC relates to a method for isolating a compound that modulates the CC expression of a nucleic acid sequence operably linked to a gene promoter, CC cell growth or viability. The methods are used to detect genes that are essential for the growth and viability of organism. Such genes can be CC used e.g. as targets for anti-microbial therapy
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                             TACAAGCGCGGTTTGTATCAAGACCGTGTAGCAGCAAAATAGGGTAGTTAG
                                                                                           ATGGGGCAAATCCTCTCCTTACCTATGGTGATCATCGGTATTTTGATGATGGTTTGGTCT
                                                                                                                               ATAGTCGAGTTCTTCCGCCAACCAGATGCACAACTGGGCTTATTCGACGGGATCAGT---
                                                                                                                                                                                                                                                                                               TATGAATTCGCCTTAGAAGGCGTGGTTCTTGTTCTTTATTCTTAATTGGTTAATTGGTAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                CCTTGGGCTTTTGTATTCCCTA--
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TATAAACACCAAGGTAATAAGGTACAAGGTAAAATGAAACAGTATCTGG
                                                            ATGGGGCAAATTCTTTCTATACCAATGATCCTGGCGGGAATATTAATGATGATATGGGCA
                                                                                                                                                              CTTGTGGAATACGTCCGTGAGCCAGATGCTCAGTTGGGTCTGTTTGGTGGCTTCATTTCA
                                                                                                                                                                                             CCTCGCCCAATGGGCAGTGTTTCCGGGTTTATTCTTAATTGGCTACGGTATTTTCCGAGTG
                                                                                                                                                                                                                               CCTCGTCCGCTAGGCAGCGTATCCGGACTGTTTTTAGCTGGATACGGTACATTCCGCTTC
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Pred. No. 4.8e-76;
0; Mismatches 278
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RESULT 13
ACF65386_0
WP Sequence split into
WP Fragment Name

7

fragments Begin

LOCUS End

ACF65386

Accession Acf65386

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14 ATGCCTCAGGGTTATCTGCAGTTTCCCAATATTGACCCCGTATTGTTTTCGATCGGCCCT

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Query Match
Best Local Similarity
Matches 544; Conser

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Score 278.2; DB 7; Pred. No. 4.8e-76; 0; Mismatches 278;

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Sequence

700779

BP; 190440 A; 140977 C; 164444 G;

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1 Other;

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ACF65386_0
ACF65386_1
ACF65386_2
ACF65386_3
ACF65386_4
ACF65386_5
ACF65386_6
ACF65386_6
                         response or sensitivity to toxins and antibiotics produced by P. Iuminescens. Cells transformed to express the genes are useful for recombinant production of the proteins, particularly toxins and antibacterials useful as insecticides, bactericides and fungicides. The genes, proteins, vectors containing the genes and Ab are also useful therapeutically (to treat microbial infection by bacteria or fungi that are sensitive to P. luminescens-encoded toxins or antibiotics) and as biopseticides. Other uses of the genes and the proteins are as virulence factors and for identifying targets of human diseases for which P. luminescens is a model (particularly plague and whooping cough). This sequence represents one of the isolated P. luminescens genes
                                                                                                                                                                                                      The invention relates to the isolation of genes and their encoded proteins from Photorhabdus luminescens. The isolated sequences are sources of probes and primers for detecting the genome of P. luminescens and related species; to study polymorphisms; for gene analysis and for detection/amplification of the genes. Antibodies (Ab) raised against the polypeptides encoded by the genes are used for detection/identification of P. luminescens, e.g. in foods. The genes, proteins, Ab and cells that carry a gene-containing vector are used to select compounds that carry a gene-containing vector are used to select compounds that modulate, regulate, induce or inhibit expression of the genes in plants, animals or microorganisms other than P. luminescens and are able to alter
                                                                                                                                                                                                                                                                                                                                                                                                                    Genomic sequence of Photorhabdus luminescens useful e.g. as therapeutic antimicrobials and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     detection; food; gene expression; plant; animal; microorganism; toxin; antibiotic; biopesticide; virulence factor; disease model; plague; whooping cough; gene; ds.
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RESULT 14
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Continuation (2 of 7) of ACF65386 1
WP Sequence split into 7 f:
WP Fragment Name
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Score 278
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  Photorhabdus luminescens nucleotide sequence
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Best Local Similarity 61.1%;
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                                                                               ATGGGGCAAATTCTTTCTATACCAATGATCCTGGCGGAATATTAATGATGATATGGGCA
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                                     TACAAGCGCGGTTTGTATCAAGACCGTGTAGCAGCAAAATAGGGTAGTTAG
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Query Match
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Matches 528
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 876 BP; 200 A; 177 C; 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             proteins from Photorhabdus luminescens. The isolated sequences are sources of probes and primers for detecting the genome of P. luminescens and related species; to study polymorphisms; for gene analysis and for detection/amplification of the genes. Antibodies (Ab) raised against the polypeptides encoded by the genes are used for detection/identification of P. luminescens, e.g. in foods. The genes, proteins, Ab and cells that carry a gene-containing vector are used to select compounds that modulate, regulate, induce or inhibit expression of the genes in plants, animals or microorganisms other than P. luminescens and are able to alter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genomic sequence of Photorhabdus luminescens useful e.g. as therapeutic antimicrobials and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antibacterial; fungicide; insecticide; polymorphium; genetic analysis; detection; food; gene expression; plant; animal; microorganism; toxin; antibiotic; biopesticide; virulence factor; disease model; plague; whooping cough; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 2; SEQ ID NO 8251; 1205pp; French.
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                                                                                                                                                                                                                                                       ATAGCCCTCCATTGGTATGGTTTCATGTACTTGGTTGGGTTTGTATTCGCCATGTGGCTA 120
                                                                                                                                                                                                                                                                                                   CTAGCGGTGCGCTATGGCTTGATGTATTTGGTGGGTTTCCTTTTTGCTATGTGGTTG 133
                                                                                                                                                                                                                                                                                                                                                                                                                           ATGCCTCAGGGTTATCTGCAGTTTTCCCAATATTGACCCCGTATTGTTTTTCGATCGGCCCT
CTTTATGCAGGTTTTGCTGGCGTATTTGTTGGTGGCCGTCTGGGCTACGTCCTGTTTTAT
                                                        TTATTCGCCGGCTTTTTAGGTGAGTGATCGGTGGCCGAGTTGGTTATGTGATCTTCTAC 253
                                                                                                                                                                                                                                                                                                                                                                                       ATGAGTAACAGCTACCTGGCATTTCCTAATATTGACCCGGTCATTTTTTCAATAGGTCCA
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TACAAGCGC 796 TATAAACAC 846 .	ATGGGGCAAATCCTCTCCTTACCTATGGTGATCATCGGTATTTTGATGATGGTTTGGTCT 787	CTTGTGGAATACGTCCGTGAGCCAGATGCTCAGTTGGGTCTGTTTGGTGGCTTCATTTCA 727	CCTCGTCCGCTAGGCAGCGTATCCGGACTGTTTTTAGCTGGATACGGTACATTCCGCCTTC 667	TATGAATTCGCCTTAGAAGGCGTGGTTCTGTTCTTTATTCTTAATTGGTTATTGGTAAA 607 		CCTTGGGCTTTTGTATTCCCTA512	ATGGGACGTATCGGTAACTTTATGAATAGTGAACTTTGGGGACGAGTAACGGATGTG 490	CAACGCACCTTCTTTGGTGTGGCCGATTTTGTTGCCCCTTTAGTGCCCATTCGGTTTGGGG 433	TCCTTCCACGGCGGCTTATTGGGTGTGATCACCGCCATGTTCTGGTATGCGCGTAAAAAC 373	AATTTTGATCTGTTCCTTGCTGACCCTCTTTATTTATTCAAAGTGTGGACTGGCGGCATG 313

Search completed: July 31, 2004, 13:34:23 Job time: 770 secs

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Result
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US-09-277-565-17

US-09-252-991A-15232

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US-09-253-61A-2365

US-09-2489-039A-2965

US-09-2489-039A-2965

US-09-290-988-1

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Sequence 17, Appl
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1.3	1.4	1.4	1.4	1.5	1.5	1.5	1.5	1.5	1.6	1.6	1.6	1.6	1.6	1.6	1.6	1.6	١.,
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14, App	293, Ap	95, App	14, App	2, Appl	3, Appli	3, Appli	1317, A	2654, A	275, App	130, Ap	17, App		17, App	1, Appl	2355, A	2884, A	

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RESULT 1
US-09-557-884-1
; Sequence 1, Application US/09557884
; Patent No. 6506581
; GENERAL INFORMATION:
; APPLICANT: Fleischmann et al.
; APPLICANT: Fleischmann et al.
; TITLE OF INVENTION: The Nucleotide sequence of the Haemophilus influenzae Rd Genome, Fragments Thereof, and Uses Thereof
                                                                                      STRANDEDNESS: double
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-557-884-1
Query Match 25.6
Best Local Similarity 66.7
Matches 1134; Conservative
                                                                                                                                                                         TELEFAX: 301-309-8439
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1830121 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/476,102

FILING DATE: JUN-5-1995

ATTORNEY AGENT INFORMATION:

NAME: Michelle S. Marks

REGISTRATION NUMBER: 41,971

REFERENCE/DOCKET NUMBER: PB186P3

TELECOMMUNICATION INFORMATION:

TELEPHONE: 301-309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: 3 1/2 inch diskett
COMPUTER: Dell Pentlum
OPERATING SYSTEM: MS DOS v6.22
SOPTWARE: ASCII Text
CURRENT APPLICATION DATA:
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ADDRESSEE: Human Genome Sciences,
STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
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                                                     GCTGAATTTTTAGGTTATATTCGTGGATATGACAATGCCGCTGATTTCCGCGCACTTGGC
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Patent No. 6528289
GENERAL INFORMATION:
APPLICANT: Robert D. Fleischmann
STATE: MD
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: 3 1/2 inch diskette
COMPUTER: Dell Pentium
OPERATING SYSTEM: MS DOS v6.22
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/09/643,990A
FILING DATE: 23-Aug-2000
CLASSIFICATION: <Unknown>
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences,
STREET: 9410 Key West Avenue
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TYPE: nucleic acid
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STRANDENNESS: double
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TOPOLOGY: linear
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SEQUENCE DESCRIPTION: SEQ ID NO:
US-09-643-990A-1
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Matches 1134; Conservative
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APPLICATION NUMBER: 08/487,429
FILING DATE: 1995-06-07
APPLICATION NUMBER: 08/426,787
FILING DATE: 1995-04-21
ATTORNEY/AGENT INFORMATION:

NAME: Kenley K. Hoover
REGISTRATION NUMBER: 40,302
REFERENCE/DOCKET NUMBER: PB186P1C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-610-5790
TELEPHONE: 301-610-5790
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                       GGTACATTCCGCTTCCTTGTGGAATACGTCCGTGAGCCCAGATGCTCAGTTGGGTCTGTTT
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Pred. No. 1.7e-245;
0; Mismatches 538;
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RESULT 3 US-09-43-681A-2282 ; Sequence 2282, Application US/09543681A ; Patent No. 6605709

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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 2282
LENCTH: 873
TYPE: DNA
ORGANISM: Proteus mirabilis
US-09-543-681A-2282
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APPLICANT: GARY BRE
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Best Local Similarity
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GCAGGATTTGGAAACTTGGGTCACTTTGGATGATTTTTGACGTCACCGGATATCAGTTCCA 1659
                                         ACTAAAAAGAGAGCCATTGCCATTACCTAAGCTACATATTAATCCAAACATTAAGACATT
                                                                             GCTAAAACGTGAGCCATTCCCAGCGCCTCAGTTCCATATCAATCCAAAGATTAAAACACT
                                                                                                                           CCATAAGATAGTTAATGCTCACATTTATGAGAACCAATTACCTCTGATGCGTGATGTTCA
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Pred. No. 5.2e-132;
0; Mismatches 287;
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APPLICANT: McKalanos, John J.
APPLICANT: Akerley, Brian J.
APPLICANT: Rubin, Eric J.
APPLICANT: Rubin, Eric J.
APPLICANT: Camilli, Andrew
TITLE OF INVENTION: SYSTEMATIC IDENTIFICATION OF ESS
TITLE OF INVENTION: GENES BY IN VITRO TRANSPOSON MUT
FILE REFERENCE: 00742/052002
CURRENT APPLICATION NUMBER: US/09/277,565
CURRENT APPLICATION NUMBER: 60/079,770
EARLIER APPLICATION NUMBER: 60/079,770
EARLIER FILING DATE: 1998-03-27
NUMBER OF SEQ ID NOS: 29
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SEQ ID NO 17
LENGTH: 807
TYPE: DNA
ORGANISM: Haemophilus influenzae
US-09-277-565-17
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US-09-277-565-17
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Patent No. 6207384
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  TAGGCAGCGTATCCGGACTGTTTTTAGCTGGATACGGTACATTCCGCTTCCTTGTGGAAT
                                                                     CCTTAGAAGGCGTGGTTCTGTTCTTTATTCTTAATTGGTTTATTGGTAAACCTCGTCCGC
                                                                                                                                                    TTGTATTCCCTAATGGTGGCC---CACTGCCGCGCCATCCTTCACCAGCTTTATGAATTCG
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                                         TTTTAGAAGGCCTGGTGTTTACGATTCTGAATATTTTTATTAAAAAACCACGTCCAA
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PRIOR APPLICATION NUMBER: US 60/09
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 15221
LENGTH: 810
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-15221
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US-09-252-991A-15221
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT FILING DATE: 1999-02-18 PRIOR APPLICATION NUMBER: US 60/074,788 PRIOR FILING DATE: 1998-02-18
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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Pred. No. 2.6e-87;
0; Mismatches 296;
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US-09-252-991A-15232
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LENGTH: 954
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACII
TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS
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AACTTTATGAATAGTGAACTTTGGGGACGAGTAACGGATGTGCCTTTGGGCTTTTGTATTC
                                       CAGCTGATGGACTTCATCGCCCCGCTGGTGCCCATCGGCCTGGGCGCCGGGCGCATCGGC
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NUCLEIC ACID AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
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Pred. No. 3e-87;
0; Mismatches 2
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US-09-252-991A-15227
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SEQ ID NO 15227
LENGTH: 1434
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
S-09-252-991A-15227
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
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Similarity 61.3%;
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CTGCTCGGCGTGATGCTGGCGGTCTGGTGGTTCGGCAAGCGCCATGGCAAGAGCTTCTTC
                          TTATTGGGTGTGATCACCGCCATGTTCTGGTATGCGCGTAAAAACCAACGCACCTTCTTT
                                                                       ATCGCCAACCCGACGCTGATCTTCGAGGTCTGGAAAGGCGGCATGTCCTTCCATGGCGGC
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SEQ ID NO 2365
LENGTH: 891
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Patent No. 6605709
GENERAL INFORMATION:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: NUCLEIC ACID AND AMINO TITLE OF INVENTION: DIAGNOSTICS AND THERAL FILE REFERENCE: 2709.1002-001

CURRENT APPLICATION NUMBER: US/09/543,681A

CURRENT FILING DATE: 2000-04-05

PRIOR APPLICATION NUMBER: US 60/128,706

PRIOR FILING DATE: 1999.04-09
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                                                                                                TTTTTAGGTGTAGTGATCGGTGGCCGAGTTGGTTATGTGATCTTCTACAATTTTTGATCTG
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TTTTTAGATAATCCACTTTACCTATTTAAAGTCTGGGATGGCGGAATGTCCTTCCACGGT
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Pred. No. 1.7e-81;
0; Mismatches 252;
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APPLICANT: GATY Breton et. al

APPLICANT: GATY BRETON: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO F

TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 2709.2004001

CURRENT APPLICATION NUMBER: US/09/489,039A

CURRENT FILING DATE: 2000-01-27

PRIOR APPLICATION NUMBER: US 60/117,747

PRIOR FILING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 14342

SEQ ID NO 2965

LENGTH: 879

TYPE: DNA

ORGANISM: Klebsiella pneumoniae
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                                                                                                                                          Score 256.8; DB 4;
Pred. No. 2.3e-78;
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                                                                         APPLICANT: Gary L. Breton et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: GTC99-03PA CURRENT APPLICATION NUMBER: US/09/328,352 CURRENT FILING DATE: 1999-06-04 NUMBER OF SEQ ID NO 3810 LENGTH: 834
                                                                                                                                                                                                                         Sequence 3810, Applia Patent No. 6562958 GENERAL INFORMATION:
Query Match
                                             TYPE: DNA ORGANISM: Acinetobacter
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        APPLICANT: SHIGENOBU, SHUJI
APPLICANT: WATANABE, HIDEMI
APPLICANT: HATTORI, MASAHIRA
APPLICANT: SAKAKI, YOSHIYUKI
TITLE OF INVENTION: GENOME DNA OF BACTERIAL
FILE REFERENCE: 081356/0159
CURRENT APPLICATION NUMBER: US/09/790,988
CURRENT FILING DATE: 2001-02-23
PRIOR APPLICATION NUMBER: JP2000-107160
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 7
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Best Local Similarity
Matches 432; Conserv
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LENGTH: 640681
TYPE: DNA
ORGANISM: Buchnera
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                                                                                                                      TCCGGACTGTTTTTAGCTGGATACGGTACATTCCGCTTCCTTGTGGAATACGTCCGTGAG
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CCTATGATTATTGCTGGATTAATTATTATGTATAAATCTTA
                             CCTATGGTGATCATCGGTATTTTGATGATGGTTTTGGTCTTA
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Pred. No. 1.2e-39;
0; Mismatches 323;
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RESULT 12
US-09-540-236-663
; Sequence 663, Application
; Patent No. 6673910
; GENERAL INFORMATION:

US/09540236

APPLICANT: Gary L.

Breton

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US-09-596-002-35; An
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US-09-540-236-663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: 2709.2005-001
CURRENT APPLICATION NUMBER: US/09/540,236
CURRENT FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 3840
SEQ ID NO 663
                                                                                                                                                                                                                                                                         sequence 35, Application US/09596002
Patent No. 6632636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 263; Conserv
                                                                                               SOFTWARE:
SEQ ID NO 35
                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                               TITLE OF INVENTION: NUCLEOTIDE SEQUENCES PILE REFERENCE: PM-0008-4 US CURRENT APPLICATION NUMBER: US/09/596,002 CURRENT FILING DATE: 2000-06-16
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte template ID
PUBLICATION INFORMATION:
                                                                                                                                       PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 1999-
                                                                                                                                                                                                                      APPLICANT:
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                                                                                                                          NUMBER OF SEQ ID NOS:
                                                       ORGANISM: M. catarrhalis
                                                                     TYPE: DNA
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                                            FEATURE:
                                                                                 LENGTH: 96109
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Berg, Kim, L.
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                                                                                                                                                                                                                                                   Robert,
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Pred. No. 5.4e-39;
0; Mismatches 177;
                                                                                                                                                                                                                                                                                                                                                             467
                 No.
                                                                                                                                                                                                         OF MORAXELLA CATARRHALIS GENOME
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RESULT 14
US-09-252-991A-15244/c
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                                                             GENERAL INFORMATION:
APPLICANT: Marc J.
                                                                                                    Patent No. 6551795
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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                                                                                                                                                                                                                                                                                                                                       AATAGTGAACTTTGGGGACGAGT 480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCTCTTTATTTATTCAAAGTGTGGACTGGCGGCATGTCCTTCCACGGCGGCTTATTGGGT 337
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59.1%;
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US-09-252-991A-15244
                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 15244
LENGTH: 435
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
                                      TATGGCTTGATGTATTTGGTGGGTTTCCTTTTTGCTATGTGGTTGGCCAATCGCCGAGCG
TACGGGCTGATGTACCTGATCGGGATCGGCGGCGCCTGGCTGCTGGCGTCGCGCCGGATG
                                                                                   CTGACGTATCCCCAGATCCGGTTGCGCTGGCCATCGGCCCGCTGAAGATCCACTGG
                                                                                                                            CTGCAGTTTCCCAATATTGACCCCGTATTGTTTTCGATCGGCCCTCTAGCGGTGCGCTGG
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                                                                                                                                                                                         Score 115; DB 4;
Pred. No. 3.3e-29;
                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                Length 435;
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                                          148
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TELEX: 846169
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2288 base pairs
TYPE: nucleic acid
; TYPE; nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-08-935-433-1
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US-08-935-433-1/c
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Patent No. 6319688
GENERAL INFORMATION:
                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                        TELEPAX: 610-407-0701
TELEX: 846160
                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UDMBER: 60/044
APPLICATION UDMBER: 70/044
FILING DATE: 28-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: PRESTIA, PAUL F
REGISTRATION NUMBER: 23,03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA: APPLICATION MADEER: US/08/935,433 FILING DATE: 23-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
COMPUTER: IBM Compat
OPERATING SYSTEM: DO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: RATNER & PRESTIA
STREET: P.O. BOX 980
CITY: VALLEY FORGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: A HUMAN SODIUM DEPENDENT PHOSPHATE TITLE OF INVENTION: TRANSPORTER (IPT-1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
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                          ACTGGCGAAAGCACGGCGAAACTCTTCTTTACAGCGCATATGGCCCAAGGCTGACGAGAGT
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TCCTGCAAAAGCTCTTCTGAACTCACTCCGATCTCCCACCTGCATGAGCGCAACAATAGT
                                                                 CACCTCCACGGGCAAGAGCACCAACACGGACAGCCAGTTGAAGAAGTCATGGACAGTGGC
                                                                                                 CATTTCTAGAGGTAGGAAGATCAGCACCGCGAGAAGATTGAAAAAATCGTGGATGGTGGC
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                                                                                                                                 Score 75.4; DB 4;
Pred. No. 7.8e-15;
0; Mismatches 126;
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Search completed: July 31, 2004, 17:02:39 Job time : 160 secs

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Perfect score:
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                                                                                                                                                                                                                                                                                                                   Published Applications NA:*

1: /cgn2_6/ptodata/2/pubpna/USO7_PUBCOMB.seq:*

2: /cgn2_6/ptodata/2/pubpna/USO7_NEW_PUB.seq:*

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Gapop·10.0 , Gapext 1.0
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score 1112.6 842.4 744.2 744.2	Mat cl	n Length D 	DB 13 13 13 13	DB ID 13 US-10-282-122A-40937 13 US-10-282-122A-40936 15 US-10-329-960-1 16 US-10-329-670-1	
	1112.6		1149	13	US-10-282-122A-4093	7
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v	505.4	17.	852	13	US-10-282-122A-30692	92
6	462.2		852	13	US-10-282-122A-22162	162
7	403.8		849	13	US-10-282-122A-32325	325
89	248.2		876	9	US-09-741-669-182	
9	152.2	ن .	540681	9	US-09-790-988-1	
10	142.2	4.9	96109	ω	US-10-672-787-35	
c 11	115.4	4.0	2731748	17	US-10-297-465A-1	1
c 12	84	2.9	2440	12	US-10-152-319A-1	589
c 13	77.8	2.7	3950		12 US-10-152-319A-1988	886
C 14	75.4		2208		US-10-276-774-13	31

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US-10-283-975-209 US-10-240-965-200 US-99-741-669-181 US-10-282-122A-6574 US-09-738-626-942 US-09-954-139-1 US-09-987-446-1 US-09-987-446-1 US-10-282-122A-14234	S-10 S-10 S-11	US-10-282-122A-33224 US-10-282-122A-42178 US-10-282-122A-14737 US-10-282-122A-12730 US-10-332-859-254	US-10-169-395-81 US-10-108-260A-1011 US-09-738-626-3017 US-10-627-476-511 US-09-738-626-1	S-10 S-10 S-10 S-10
-10-283-975A-254 -10-240-965-200 09-741-669-181 -10-282-122A-657 09-738-626-94-2 09-738-626-94-2 09-987-446-1 -10-282-122A-142	-10-084-817-332 -09-877-178-11 -10-342-887-556 -10-172-118-556 -10-388-360-350 -10-159-563-244	-10-282-122A-33224 -10-282-122A-42178 -10-282-122A-14737 -10-282-122A-12730 -10-282-122A-12730 -10-332-859-254	0-16 -738 -738	10-173-999-149 10-116-802-36 1-10-052-664-2 10-257-021-146 10-097-340-220 10-404-460-258 10-169-395-71
33-62 33-62 3-62 3-62	777-1	22222	8-62	9-1-1
3757 39-3 59-3 1227 126-9 136-3	178- 178- 118- 160-	1221 1221 1221 1221 139-	26-3	95-
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Sequence 254, App Sequence 200, App Sequence 181, App Sequence 6574, Ap Sequence 942, App Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli	111, 556, 350, 244,	33224, 42178, 14737, 12730, 254, A	11, 1, Ap	149, App 36, Appl 2, Appli 146, App 220, App 258, App 71, Appl
Sequence 254, App Sequence 200, App equence 181, App Sequence 6574, App equence 942, App equence 1, Appli equence 1, Appli equence 1, Appli Sequence 14234, A	332, App 11, Appl 556, App 556, App 350, App 244, App	33224, A 42178, A 14737, A 12730, A 254, App	81, Appl 1011, Ap 3017, Ap 511, App 1, Appli	149, App 36, Appli 2, Appli 146, App 220, App 258, App 71, Appl
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ALIGNMENTS

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PRIOR	PRIOR	PRIOR	PRIOR	SOL 2d	PRIOR	PRIOR	PRIOR	PRIOR	PRIOR	PRIOR	PRIOR	PRIOR	PRIOR	CUR	CUR	FIL	TIT	APP	APP	APP	APP	APP	APP	APP	APP	APP	APP	APP	APP	GENERAL INFORMATION:	Publication No. US20040029129AJ	Sequence	RESULT 1
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PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper NUMBER OF SEQ ID NOS: 78614
SOFTWARE: Patentin version 3.1
SEQ ID NO 40937
LENGTH: 1149
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Best Local Similarity
Matches 1118; Conserv
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FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
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PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PILING DATE: 2000-10-2
PRIOR PILING DATE: 2001-02-09
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Wall, Daniel
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Yamamoto, Robert
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
                                                                                 SOFTWARE: PatentIn version
SEQ ID NO 40936
LENGTH: 852
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                                                                                                                                                                   Remaining Prior Application data removed NUMBER OF SEQ ID NOS: 78614
                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/269,308 PRIOR FILING DATE: 2001-02-16
                        TYPE: DNA ORGANISM: Vibrio cholerae
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Query Match Best Local Similarity

29.0%;

Score Pred.

842.4; DB 13; No. 1.2e-267;

Length 852;

GROANCOGRATTITHANTETTTOTACCGARTCCANGGATTCANGGTTGANAT 898	RESULT 3 US-10-329-960- US-10-329-960- ; Sequence 1, ; Publication ; GEMERAL INFO ; APPLICANT: ; TITLE OF IN ; TITLE OF IN ; TITLE OF IN ; FILE REFERE ; CURRENT APP	당 왕	문 왕	Db Qy	D 40	망 왕	B 8	B 8	g Qy	B 8	B 8	B Q	B 8	B 8	B 8	р Q
898 60 958 1120 1018 11078 1240 11078 240 11198 360 11258 420 11318 480 1378 1378 1498 660 1498 660 11618 1618 1618 1618 1618 1678 1678 167	1 Application US/10329960 No. US20030099277A1 RMATION: Fleischmann et al. VENTION: Mucleotide Sequence of the Haemophilus VENTION: Thereof, and Uses Thereof NCE: PB186P1 LICATION NUMBER: US/10/329,960	TTTTCAGTCTAA TTTTCAGTCTAA	GTCACTTTGGATGATTTTGACGTCACCGGATATCAGTTCCACGATCCTAT			439 601										
ri ag	R d				CATTC 155	149	143 600			125	119 360	113 300		101 180		

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WG DATE: 2003-01-02
VITION NUMBER: US 09/643,990
DATE: 2000-08-23
VITION NUMBER: US 08/487,429
DATE: 1995-06-07
VITION NUMBER: US 08/426,787
DATE: 1995-04-21
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1905)..(44905)
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)808)..(40810)
\TION: n equals {
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5551)..(36551)
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j543)..(36543)
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)150)..(10150)
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)21)..(9921)
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732)..(45732)
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975)..(44975)
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)36)..(47036)
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FEATURE:

NAME/KEY: misc_feature
LOCATION: (122336)..(122336)
OTHER INFORMATION: n equals
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LOCATION: (121344)..(121344)
OTHER INFORMATION: n equals
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LOCATION: (119924)..(119924)
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LOCATION: (117136)..(117136)
OTHER INFORMATION: n equals
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LOCATION: (105121)..(105121)
OTHER INFORMATION: n equals
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LOCATION: (65309)..(65309)
OTHER INFORMATION: n equals
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LOCATION: (55369)..(55369)
OTHER INFORMATION: n equals
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NAME/KEY: misc_feature
LOCATION: (51602)...(51602)
OTHER INFORMATION: n equals
                                             LOCATION: (122167)
OTHER INFORMATION:
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LOCATION: (120038)..(120038)
OTHER INFORMATION: n equals
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LOCATION: (102696)..(102696)
OTHER INFORMATION: n equals
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LOCATION: (100091)..(100091)
OTHER_INFORMATION: n equals
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LOCATION: (51805)...(51805)
OTHER INFORMATION: n equals
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LOCATION: (51786)..(51786)
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LOCATION: (65313)..(65313)
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LOCATION: (107248)..(107248)
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LOCATION: (80024)..(80
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(122167)..(122167)
ORMATION: n equals
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(119750)..(119750)
ORMATION: n equals
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LOCATION: (152500)..(152500)
OTHER INFORMATION: n equals
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LOCATION: (150841)..(150841)
OTHER INFORMATION: n equals
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NAME/KEY: misc_feature
LOCATION: (145058)..(145058)
OTHER INFORMATION: n equals
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LOCATION: (139910)..(139910)
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NAME/KEY: misc feature
LOCATION: (131360)..(131360)
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LOCATION: (131340)..(131340)
OTHER INFORMATION: n equals
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LOCATION: (147197)..(147197)
OTHER INFORMATION: n equals
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LOCATION: (145942)..(145942)
OTHER INFORMATION: n equals
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LOCATION: (145171)..(145171)
OTHER_INFORMATION: n equals
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LOCATION: (142750)..(142750)
OTHER INFORMATION: n equals
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LOCATION: (140398)..(140398)
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LOCATION: (152530)..(152530)
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GTGTGGACTGGCGGCATGTCCTTCCACGGCGGCTTATTGGGTGTGATCACCGCCATGTTC
                                                                                                           GAGCAAGTCTCTGACTTGTTATTCGCCGGCTTTTTAGGTGTAGTGATCGGTGGCCGAGTT
                                                                                                                                                                                              ACGCTTGGCGATAGTAATATCGGCTTACGTTATGGTATGGCTTGATGTACCTTTTAGGTTTT
                                                                                                                                                                                                              TCGATCGGC-----CCTCTAGCGGTGCGCTGGTATGGCTTGATGTATTTGGTGGGTTTC 115
                                                                                                                                                                                                                                                 ATAAGGAAAATTATGAATTCAAATTATTTACTTCTTCCCCCACTTTGATCCGAGTATTTTT 958145
                                                                                           GATCAAGTTGATAGCTTACTTTTCAACGGTTTTTATGGGGGGTGTTTATTGGCGGACGTGTT
                                                                                                                                           GTTTTTGCACGTTGGCTTGCGGTTCGCCGTGCTAATCGCCCCAAATAGCGGTTTGGACAGTA 958265
                                                                                                                                                              CTTTTTGCTATGTGGTTGGCCAATCGCCGAGCGGATCGCGCGGGCAGTGGTTGGACGCGT 175
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                                         Conservative
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Pred. No. 1.4e-232;
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blication No. US20040018503A1
MERAL INFORMATION:
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MERAL INFORMATION:
MITTLE OF INVENTION: Nucleotide Sequence of the Haemophilus influenzae Rd Genome, Fray
MITTLE OF INVENTION: Thereof, and Uses Thereof
MITTLE OF INVENTION:
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LOCATION: (102696)..(102696)
OTHER INFORMATION: n equals
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LOCATION: (100091)...(100091)
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NAME/KEY: misc feature
LOCATION: (80024)..(80024)
OTHER INFORMATION: n equal
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LOCATION: (51786)..(51786)
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LOCATION: (51334)..(51334)
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LOCATION: (44975)...(44975)
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LOCATION: (44905)...(44905)
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LOCATION: (44416)..(44416)
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LOCATION: (105121)...(105121)
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LOCATION: (65313)..(65313)
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LOCATION: (145942)..(145942)
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LOCATION: (147197)..(147197)
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Best Local Similarity 66.7%;
Matches 1134; Conservative
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OTHER INFORMATION: n equals
FEATURE:
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                                                                                                                                                                                                                                                                  Sequence 30692, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
                             APPLICANT:
APPLICANT:
TITLE OF I
                                                                                                    APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                       APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
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f: Xu, H.
INVENTION: Identification of Essential
ERENCE: ELITRA.034A
                                                                        Trawic.,
Carr, Grant
Camoto, Robert
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                                                               Yamamoto, ku
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SOFTWARE: Patentin version 3.1
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DR FILING DATE: 2000-09-09

DR APPLICATION NUMBER: 60/242,578

DR FILING DATE: 2000-10-23

DR APPLICATION NUMBER: 60/253,625

DR FILING DATE: 2000-11-27
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FILING DATE: 2000-12-22
APPLICATION NUMBER: 60/267,636
FILING DATE: 2001-02-09
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FILING DATE: 2000-09-06
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                                                                                             TGTACAGCCATCATTTTTCATTGCTGGGGGATACCTTGTATCTCAACAGTACTCAGCGTT
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PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
                                                               Remaining Prior Application data removed
NUMBER OF SEQ ID NOS: 786.4
SOFTWARE: PatentIn version 3.1
SEQ ID NO 22162
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PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Identification of Essential Genes FILE REFERENCE: ELITRA.034A CURRENT APPLICATION NUMBER: US/10/282,122A CURRENT FILING DATE: 2003-02-20 PRIOR APPLICATION NUMBER: 60/191,078 PRIOR FILING DATE: 2000-03-21 PRIOR APPLICATION NUMBER: 60/206,848
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PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
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TYPE: DNA ORGANISM: Haemophilus influenzae
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Zyskind, Judith
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Malone, Cheryl
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Yamamoto, Robert
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                                                  Sequence 32325, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
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Best Local Similarity 71.4%;
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APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
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Pred. No. 1.7e-141;
0; Mismatches 243;
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US-10-282-122A-32325
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PRIOR PILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR PILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2000-12-26
PRIOR PILING DATE: 2000-12-26
PRIOR PILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-16
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Best Local Similarity
Matches 570; Conserv
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PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data remu
NUMBER OF SEQ ID NOS: 78614
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CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
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                                   GTCATATTGACCAGTTGAAAAAGATTGTTGATGATTTGAGCCGTTGGCGTTGATGACCGAG
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     AACGGACAGGAACCCGTTGTTTAACGGTGATAAATGCCGATCTGGAATATGATGTTGCCA
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                                                                       AAGATGATATGGGCCGAGTCTATGGTGTTCAAGGACGCCAATGGCAACGCCCTGATGGCT
                                                                                                          AGGATGACATGGGACGCGTGTATGGTGTTCAGGGTAGAGCTTGGGCTAAGCCTGATGGTG
                                                                                                                                            CGTGGAACGCGAATGCTAATGAAAATAGCGCATGGTTAAATAATCCGCATCGTAAGGGTG
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Wall, Dar
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Pred. No. 4e-1:
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APPLICANT: Forsyth, R. Allyn
APPLICANT: Ohlsen, Kari L.
APPLICANT: Cyskind, Judith W.
TITLE OF INVENTION: Genes identified as required for TITLE OF INVENTION: proliferation of E. coli FILE REFERENCE: ELITRA.009A
CURRENT APPLICATION NUMBER: US/09/741,669
CURRENT FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: US 60/173005
PRIOR FILING DATE: 1999-12-23
NUMBER OF SEQ ID NOS: 481
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(876)
US-09-741-669-182
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US-09-741-669-182
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TYPE: DNA
ORGANISM: Escherichia
                                                                                                                                                                                                                                                                                                                                                         Match 8.5%;
Local Similarity 58.8%;
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                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                            Score 248.2; DB 9;
Pred. No. 1.7e-70;
0; Mismatches 288;
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                                                                                            FILE REFERENCE: 081356/0159
CURRENT APPLICATION NUMBER: US/09/790,988
CURRENT FILING DATE: 2001-02-23
PRIOR APPLICATION NUMBER: JP2000-107160
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 7
SOPTWARE: PATENTIN Ver. 2.1
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 9
US-09-790-988-1
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Patent No. US2002217687A1
GENERAL INFORMATION:
APPLICANT: SHIGENOBU, SHUJI
APPLICANT: WATANABE, HIDEMI
APPLICANT: HATTORI, MASAHIRA
APPLICANT: SAKAKI, YOSHIYUKI
TITLE DETERMINE SAKAKI, YOSHIYUKI
TITLE DETERMINE ANALI, WASHIYUKI
TITLE DETERMINE ANALI, WASHIYUKI
TITLE DETERMINE ANALI, WOSHIYUKI
TITLE DETERMINE ANALI, WOSHIYUKI
TITLE DETERMINE ANALI WOSHIYUKI
TITLE WOSHIYUKI WOS
LENGTH: 640681
TYPE: DNA
ORGANISM: Buchnera sp.
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RESULT 10
US-10-672-787-35
; Sequence 35, Application US/10672787
; Publication No. US20040067554A1
; GENERAL INFORMATION:
; APPLICANT: LAGACE, Robert, E.
; APPLICANT: PATTERSON, Chandra
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
APPLICANT: PATTERSON, Chandra
APPLICANT: BERG, Kim, L.
TITLE OP INVENTION: NUCLEOTIDE SEQUENCES
FILE REFERENCE: ELITRA.025C1
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                                                                                                                                                                                                                                                                                                                                                          ATTCTTCTGTTTTTTATAATTTTTTTTTTTCGAAAAAAGATAGACCAACAGGTAGTATT 479963
                                                                                                                                                                                                                                                                                                                                                                            GTGGTTCTGTTCTTTATTCTTAATTGGTTATTGGTAAACCTCGTCCGCTAGGCAGCGTA
                                                                                                                                                                                                                                                                                                                                                                                                                   AATTCTCAAAATCAAGATTTAAAAGAAATAAAAAAATATCCCCGAATTACAACTATTATTA 479843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTAATAGTGAACTATGGGGTCGTGTATCACCCAATTTTTCATATGCAATGATTTTTCCC
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                                                                                                                                                                                                        CCTATGGTGATCATCGGTATTTTGATGATGGTTTGGTCTTA 789
                                                                                                                                                                                                                                    CCAGATCCACAAATAGGACTATTAAAAAATATAATTACTATGGGACAAATATTATCACTT 480083
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Pred. No. 1.7e-36;
0; Mismatches 323;
             OF MORAXELLA
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CURRENT APPLICATION NUMBER: US/10/672,787
CURRENT FILING DATE: 2003-09-26
PRIOR APPLICATION NUMBER: 09/596,002
PRIOR FILING DATE: 2000-06-16
NUMBER OF SEQ ID NOS: 41
SOFTWARE: PERL Program
SEQ ID NO 35
LENGTH: 96109
TYPE: DNA
ORGANISM: Moraxella catarrhalis
US-10-672-787-35
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Matches
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Best Local Similarity
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                                                                                                                                                                                                        GTGATCACCGCCATGTTCTGGTATGCGCGTAAAAAACCAACGCACCTTCTTTGGTGTGGCC 397
                                                                                                                                                                                                                                                                                                                                                     ATTTTAGGTGGCCGTATTGGCTATGTACTTTTATACAATTTTTGGTGAGCTGATTGCTAAC 5136
                                                                                                                                                                                                                                                                                                                                                                                GTGATCCGTGGCCGAGTTGGTTATGTGATCTTCTACAATTTTTGATCTGTTCCTTGCTGAC
                                                                                                                          GATTTTGTTGCCCCTTTAGTGCCATTCGGTTTGGGGATGGGACGTATCGGTAACTTTATG 457
                                                                                                                                                                                                                                                                                              CCTCTTTATTTATTCAAAGTGTGGACTGGCGGCATGTCCTTCCACGGCGCTTATTGGGT 337
AATGGCGAGCTTTGGGGACGAAT 51569
                                           AATAGTGAACTTTGGGGACGAGT 480
                                                                                      GATTTTATCGCACCCTGTGTACCAACAGGCTTATTTTTTGGGCGAATTTGGGAATTTCATC
                                                                                                                                                                          GTGTTGCTTGCCATGTGGTATTTTGCACATAAATATAAAAAAGCACCCTTTACGGTACTG
                                                                                                                                                                                                                                                              CCTTTATATCTTTTTCGAGTATGGGAAGGGGGCATGAGTTTTCATGGTGGATTTGTGGGC 51426
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ilarity 59.1%;
Conservative
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Pred. No. 8.5e-34;
0; Mismatches 178
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RESULT 11
US-10-297-465A-1/c
Sequence 1, Application US/10297465A
Publication No. US20040142413A1
GENERAL INFORMATION:
APPLICANT: Simpson, Andrew
APPLICANT: Setubal, Joao
APPLICANT: Setubal, Joao
APPLICANT: Medianis, Joao
APPLICANT: Arruda, Paulo
TITLE OF INVENTION: Isolated Genome of Xylella Fastidiosa and Uses Thereof
FILE REFERENCE: FAPESP 202 US (10213376)
CURRENT APPLICATION NUMBER: US/10/297,465A
CURRENT APPLICATION NUMBER: DCT/IB01/01618
PRIOR FILING DATE: 2001-06-07
PRIOR APPLICATION NUMBER: 60/209,906
PRIOR FILING DATE: 2001-06-07
PRIOR APPLICATION NUMBER: 60/209,906
PRIOR FILING DATE: 2001-06-17
NUMBER OF SEQ ID NOS: 1
SOPTWARE: PatentIn version 3.2
SEQ ID NO 1
LENGTH: 2731748
TYPE: DNA
ORGANISM: Xylella fastidiosa
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RESULT 12
US-10-152-319A-1589/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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CURRENT APPLICATION NUMBER: US/10/152,319A
CURRENT FILING DATE: 2002-05-22
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APPLICANT: Porter, Mark
APPLICANT: Johnson, Kory
                                                                                                                                                                                                                                PRIOR PRIOR
                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Higgs, Brandon
APPLICANT: Castle, Arthur
APPLICANT: Elashoff, Michael
TITLE OF INVENTION: Molecular Toxicology Modeling
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                 DR FILING DATE: 2001-07-10

R APPLICATION NUMBER: US 60/303,807

DR FILING DATE: 2001-07-10

DR APPLICATION NUMBER: US 60/303,808

DR FILING DATE: 2001-07-10

DR APPLICATION NUMBER: US 60/315,047

DR APPLICATION NUMBER: US 60/315,047

DR FILING DATE: 2001-08-28
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                                                                                                                                                                                    APPLICATION NUMBER: US 60/297,523
FILING DATE: 2001-06-13
APPLICATION NUMBER: US 60/298,925
FILING DATE: 2001-06-19
                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 60/292,335 FILING DATE: 2001-05-22
APPLICATION
                                                                                                                                                                     APPLICATION NUMBER: US 60/303,810
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NUMBER: US
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60/324,928
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Pred. No. 8e-
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; OTHER INFORMATION:
US-10-152-319A-1589
               PRIOR APPLICATION NUMBER: US 60, PRIOR FILING DATE: 2001-07-10 PRIOR APPLICATION NUMBER: US 60, PRIOR APPLICATION NUMBER: US 60, PRIOR APPLICATION NUMBER: US 60, PRIOR FILING DATE: 2001-07-10 PRIOR APPLICATION NUMBER: US 60, PRIOR FILING DATE: 2001-09-27 PRIOR FILING DATE: 2001-09-27
                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 60/298,925
PRIOR FILING DATE: 2001-06-13
PRIOR FILING DATE: 2001-06-19
PRIOR FILING DATE: 2001-06-19
PRIOR APPLICATION NUMBER: US 60/303,810
PRIOR APPLICATION NUMBER: US 60/303,800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1589
LENGTH: 2440
TYPE: DNA
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Publication No. US20040072160A1
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                      FILE REFERENCE: 44921-5089-US
CURRENT APPLICATION NUMBER: US/10/152,319A
CURRENT FILING DATE: 2002-05-22
PRIOR APPLICATION NUMBER: US 60/292,335
PRIOR FILING DATE: 2001-05-22
PRIOR APPLICATION NUMBER: US 60/297,523
PRIOR APPLICATION NUMBER: US 60/297,523
PRIOR FILING DATE: 2001-06-13
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PRIOR APPLICATION NUMBER: US 60/330,867
PRIOR FILING DATE: 2001-11-01
PRIOR APPLICATION NUMBER: US 60/330,462
PRIOR FILING DATE: 2001-10-22
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                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Molecular Toxicology Modeling
                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Rattus norvegicus
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Local Similarity 58.5%;
                                                           FILING DATE: 2001-07-10
APPLICATION NUMBER: US 60/315,047
FILING DATE: 2001-08-28
                   APPLICATION NUMBER: US 60/324,928 FILING DATE: 2001-09-27
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Castle, Arthur
Elashoff, Michael
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  NUMBER:
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US 60/330,867
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Pred. No. 1.1e-15;
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                                                                                                                                                                                                                                                                         ; SOPTWARE: Custom
; SEQ ID NO 1331
; LENGTH: 2208
; TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1331, Application US/10276774
Publication No. US20040053245A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE: 2001-10-22
Remaining Prior Application data removed
NUMBER OF SEQ ID NOS: 2221
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1988
LENGTH: 3950
                                                                                                                                                                           Query Match
Best Local
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Best Local Similarity
                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Homo sapiens
-10-276-774-1331
                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/276,774
CURRENT FILING DATE: 2002-11-18
PRIOR APPLICATION NUMBER: 09/560,875
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: 09/496,914
PRIOR PILING DATE: 2000-02-03
NUMBER OF SEQ ID NOS: 2700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Hyseq, Inc.
APPLICANT: Tang, Y. Tom et al
TITLE OF INVENTION: No. US20040053245Alel Nucleic Acids
FILE REFERENCE: 21272-030
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                                                                                                                                                     / Match 2.6%;
Local Similarity 56.0%;
les 164; Conservative
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TCCTGCAAAAGCTCTTCTGAACTCACTCCGATCTCCCACCTGCATGAGCGCAACAATAGT
                                  ACTGGCGAAAGCACGGCGAAACTCTTCTTTACAGCGCATATGGCCAAGGCTGACGAGAGT
                                                                         CACCTCCACGGGCAAGAGCACCAACACGGACAGCCAGTTGAAGAAGTCATGGACAGTGGC
                                                                                                                CATTTCTAGAGGTAGGAAGATCAGCACCGCGAGAAGATTGAAAAAATCGTGGATGGTGGC 2535
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                                                                                                                                                                       Score 75.4; DB 13;
Pred. No. 7.6e-13;
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Pred. No. 1.9e-13;
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APPLICANT: Bos Biotechnology, Inc.
TITIE OF INVENTION: Methods of Diagnosis of Ovarian Cancer, Compositions
TITLE OF INVENTION: and Methods of Screening for Modulators of Ovarian
TITLE OF INVENTION: Cancer
FILE REFERENCE: 018501-002420US
CURRENT FILING DATE: 2002-06-17
PRIOR APPLICATION NUMBER: US/10/173,999
CURRENT FILING DATE: 2002-06-17
PRIOR APPLICATION NUMBER: US 60/299,234
PRIOR APPLICATION NUMBER: US 60/299,234
PRIOR FILING DATE: 2001-06-18
PRIOR FILING DATE: 2001-06-18
PRIOR APPLICATION NUMBER: US 60/315,287
PRIOR PRIOR DATE: 2001-08-27
PRIOR APPLICATION NUMBER: US 60/315,287
PRIOR PILING DATE: 2001-08-27
PRIOR PILING DATE: 2001-04-12
NUMBER OF SEQ ID NOS: 163
COCTUMED DATE: 2001-04-12
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SEQ ID NO 149
LENGTH: 2280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 149, Application US/10173999
Publication No. US20040005563A1
GENERAL INFORMATION:
APPLICANT: Mack, David H.
APPLICANT: Gish, Kurt C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 2476 CATTTCTAGAGGTAGGAAGATCAGCACCGCGAGAAGATTGAAAAAATCGTGGATGGTGGC
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                                                                                                   GAGCAATGAAGAGGACACCATGCTGACAACGATGGACGTTGAAGGTGCTGGAGCTCTGCAC
                                                                                                                                                                                                                                                ATTGGTCACAGTAGTACCAATATTGGCACCCATCACCATAGGAATCGCGGTTTCAACCG-
                                                                                                                                                                                                                                                                                                    TCCTGCAAAAGCTCTTCTGAACTCACTCCGATCTCCCACCTGCATGAGCGCAACAATAGT
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CAAGACGGTCACCAGCACCCCGATCACCAGCCCCAACAAAGGGTTGGACATAA
                                               --GTAACCCACCGGCAACGAGACCAACAATAATAGAAGTCACCGTGCTTGAGGATTGAAT 2712
                                                                                                                                                                                                 GTTGGTGATTGACGTTCCAATGTTGGCCCCCCATGATAATGGGGATGGCAGCCCGAACAGT
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Pred. No. 7.7e-13;
0; Mismatches 126;
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Search completed: July 31, 2004, 19:10:09 Job time: 903 secs

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Minimum
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18003.955 Million cell updates/sec
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BM924499 ACENCOIDT	BM934499	- I	1001		٠:	
	BF782519	3 :	952		٥ :	4
AKOO4832 Mus muscu	AK004832	_ :	2486		2	
BF783860 602109784	BF783860	10	945		0	40
AK011435 Mus muscu	AK011435	11	1121			
CD330290 StrPu537.	CD330290	14	407	٠	81.4	
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UI-M-FDO	BU055160	13	748		8	
CD330233 StrPu537.	CD330233	14	528	٠		
CF995901 AGENCOURT	CF995901	14	776	•	2	
BI078307 602872658	BI078307	12	756	٠	·	υ U
CB420463 593420 MA	CB420463	14	677			
AK035663 Mus muscu	AK035663	11	3128	•	À	
	AK088134	11	2256	•	4.	
AK088606 Mus muscu	AK088606	11	2255		4.	
BY74611	BY746114	13	976		۸.	
BY746793 BY746793	BY746793	13	899		۴.	
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fi68d06	AW423104	10	683	•	8	
346545	BG732886	12	591		86.6	
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BW295886 BW295886	BW295886	13	632		89	
BW061136	BW061136	13	522		8	
hab39c07	CA589861	14	662		92.4	
CA588156 hab47g03.	CA588156	14	801		96	16
BW039194 BW039194	BW039194	13	686		96	
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w	CA475083	14	828	٠	103.2	
4 hab50c01	CA588344	14	813		င္မ	
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7 PTMM0161	CD376447	14	855	•	106.2	
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ACCESSION VERSION KEYWORDS SOURCE ORGANISM JOURNAL COMMENT RESULT 1 BZ577690 REFERENCE DEFINITION FEATURES LOCUS TITLE AUTHORS Genome Center
University of Washington
Box 352145, Seattle, WA 98
Tel: 2062216954
Fax: 2066857244 1 (bases 1 to 1128)
Spencer,D.H., Raymond,C.K., Smith,E.E., Sims,E.E., Hasting, Spencer,D.H., Kaul,R. and Olsen,M.V.
Whole-Genome-Sequence variation among multiple isolates of Psedomonas aeruginosa library
J. Bacteriol. (2002) In press
Contact: Chris K. Raymond BZ577690 1128 bp DNA linear GSS 17-DEC-2 msh2_5528.y2 msh Pseudomonas aeruginosa genomic clone msh2_5528, genomic survey sequence. Email: craymond@u.washington.edu Class: shotgun. Location/Qualifiers Pseudomonas aeruginosa Bacteria; Proteobacteria; BZ577690.1 GI:27212751 Pseudomonas aeruginosa Pseudomonadaceae; Pseudomonas. WA 98105-2145, Gammaproteobacteria; Pseudomonadales; USA Sims, E.E., Hastings, M., GSS 17-DEC-2002

Result No.

Score

Query Match Length DB

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Description

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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249.8 194.8 191.8 191.8

5.6 5.6 5.6

1128 805 853 1141

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BZ577690 BZ556310 BZ578932 BZ559267

BZ577690 msh2 5528 BZ556310 pacs1-60 BZ578932 msh2 6070 BZ559267 pacs2-164

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RESULT 2
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pacs1-60_5617.x1 pacs1-60 Pseudomonas aeruginosa genomic clone
pacs1-60_5617, genomic survey sequence.
                                BZ556310
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                                                                                                             GTACCGATGGTGCTGGCCGGCATTGGCCTGATGGTCTGG
                                                                                                                               TTACCTATGGTGATCATCGGTATTTTGATGATGGTTTTGG
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                                                                                                                                                                                                  CCAGATGCTCAGTTGGG----TCTGTTTGGTGGCTTCATTTCAATGGGGCAAATCCTCTCC
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/clone="msh2_528"
/clone_ib="msh"
/clone_ib="msh"
/note="Environmental isolate. Whole
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Pseudomonas
/mol_type="genomic DNA"
/strain="MSH"
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Pred. No. 1.9e-61;
0; Mismatches 301;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: craymond@u.washington.
Class: shotgun.
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Fax: 2066857244
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                                           CCGCGCCATCCTTCACAGCTTTATGAATTCGCCTTAGAAGGCGTGG
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                    CCGCGGCATCCCTCGCAGCTGTACCAGTTCGGCCTGGAAGGCGTGG
                                                                                                   CTTTGGGGACGAGTAACGGATGTGCCTTGGGCTTTTGTATTCCCTAATGGTGGCCCACTG
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/clone="pacs1-60_5617"
/clone lib="pacs1-60"
/note="clinical isolate 1-60 Whole
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/mol_type="genomic DNA"
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University of Washington
Box 352145, Seattle, WA 98105-2145,
Tel: 2062216954
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genomic survey
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Bacteria; Proteobacteria; Gammaproteobacteria;
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AACTITATGAATAGTGAACTITGGGGACGAGTAACGGATGTGCCTTGGGGCTTTTGTATTC
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                                           CAGCTGATGGACTTCATCGCCCCGCTGGTGCCCATCGGCCCTGGGCCCCGGGCGCATCGGC
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                                                                  GGTGTGGCCGATTTTGTTGCCCCTTTAGTGCCATTCGGTTTGGGGATGGGACGTATCGGT
                                                                                              CTGCTCGGCGTGATGCTGGCGGTCTGGTGGTTCGGCAAGCGCCATGGCAAGAGCTTCTTC
                                                                                                                       TTATTGGGTGTGATCACCGCCATGTTCTGGTATGCGCGTAAAAACCAACGCACCTTCTTT
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/mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clone lib="msh"
/note="Environmental isolate. Whole
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pacs2-164_1355, genomic survey sequence
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Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: 2062216954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        University of Washington Box 352145, Seattle, WA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Spencer, D.H., Raymond, C.K., Smith, Burns, J.L., Kaul, R. and Olsen, M.V.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fax: 2066857244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pseudomonadaceae;
                               GGCAGCGTATCCGGACTGTTTTTAGCTGGATACGGTACATTCCGCTTCCTTGTGGAATAC
                                                                                       ATGGTCTTCCCCAACGGCGCAC-GTGCCGCGCATCCCTCGCAGCTGTACCAGTTCGCC
                                                                                                                                                                                                                           CGTATCGGTAACTTTATGAATAGTGAACTTTGGGGACGAGTAACGGATGTGCCTTGGGCT
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GCCTCGGTCTCCGGCCTGTTCGTGCTGCTACGGGATCTTCCGCTTCGTTGTCGAATTC
                                                                                                                                                              TTTGTATTCCCTAATGGTGGCCCACTGCCGCGCCATCCTTCACAGCTTTATGAATTCGCC
                                                                                                                                                                                                 CGCATCGGCAACTTCATCAACTCGGAACTGTGGGGCCAAGGTCAGCGATGTGCCCCTGGGCC
                                                                                                                                                                                                                                                                 AGCTTCTTCCAGCTGATGGACTTCATCGCCCCCCTGGTGCCCATCGGCCTGGGCGCCCGG
                                                                                                                                                                                                                                                                                               ACCTTCTTTGGTGTGGCCGATTTTGTTGCCCCTTTAGTGCCATTCGGTTTGGGGATGGGA 439
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCTAATGGTGGCCCACTGCCGCCCATCCTTCACAGCTTTATGAATTCGCCTTAGAAGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AACTTCATCAACTCGGAACTGTGGGGCAAGGTCAGCGATGTGCCCCTGGGCCATGGTCTTC
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                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           shotgun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       craymond@u.washington
                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:287"
/clone="pacs2-164 1355"
/clone_lib="pacs2-164"
/clone_clinical isolate 2-164
library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /strain="2-164"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       organism="Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                  5.5%;
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                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                  Score 161; DB 28;
Pred. No. 2.7e-35;
0; Mismatches 145;
                                                                regreatectergectetteacecgeaagecacegeceace
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JOURNAL COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1375 bp DNA linear pacsl-60 4149.xl pacsl-60 Pseudomonas aeruginosa pacsl-60_4149, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         University of Washington Box 352145, Seattle, WA 98105-2145,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Whole-Genome-Sequence variation among multiple isolates Psedomonas aeruginosa library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Spencer, D.H., Raymond, C.K., Smith, E.E., Burns, J.L., Kaul, R. and Olsen, M.V.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fax: 2066857244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Chris K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; Gammaproteobacteria;
                                                                                                                                                                                                                                                                                                                            Similarity
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CTAATGGTGGCCCACTGCCGCGCCATCCTTCACAGCTTTATGAATTCGCCTTAGAAGGCG
                                                                           ACTTTATGAATAGTGAACTTTGGGGACGAGTAACGGATGTGCCTTTGGGCTTTTTGTATTCC
                                                                                                                    AGCTGATGGACTTCATCGCCCCGCTGGTGCCCATCGGCCTGGGCGCCCGGGCGCATCGGCA
                                                                                                                                                GTGTGGCCGATTTTGTTTGCCCCTTTAGTGCCATTCGGTTTTGGGGATGGGACGTATCGGTA
                                                                                                                                                                                  TGCTCGGCGTGATGCTGGCGGTCTGGTGGTTCCGCCAAGCCCCATGGCAAGAGCTTCTTCC
                                                                                                                                                                                                                TATTGGGTGTGATCACCGCCATGTTCTGGTATGCGCGTAAAAACCAACGCACCTTCTTTG
                                                                                                                                                                                                                                                TTCCTGCAGCCCCGCTGATTTTCTAGGTCTGGAAAGGCGGCATGTCCTTCCATGGCGGCC
                                                                                                                                                                                                                                                                 TTGCTGACCCTCTTTATTTTATTCAAAGTGTGGGACTGGCGGCATGTCCTTCCACGGCGGCT
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                                                    ACTTCATCAACTCGGAACTGTGGGGCAAGGCCAGCTATGAGCCCTGGGCCATGGTCTTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        craymond@u.washington.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Pseudomonas
/mol_type="genomic DNA"
/strain="1-60"
                                                                                                                                                                                                                                                                                                                                                                                              /note="clinical isolate 1-60 Whole genomic shotgun
library."
                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="pacs1-60_4149"
/clone_lib="pacs1-60"
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K. Raymond
                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                            Score 152; DB 28;
Pred. No. 1.3e-32;
                                                                                                                                                                                                                                                                                                                Mismatches
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Best Local Similarity 59.8%;
Matches 234; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            9500 Gilman Drive, La Jolla,
Email: rcaspi@ucsd.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 406)
Caspi,R., Tebo,B.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pseudomonas putida
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
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                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence was obtained by automated sequencing of the DNA. It was NOT confirmed by sequencing the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Scripps Institution of Oceanography, UCSD 9500 Gilman Drive, La Jolla, CA 92093-0202,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9758766
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Caspi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pseudomonadaceae; Pseudomonas.
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                                                                                                                                                                                                                                                                                                                                                                                                           Therefore, some mistakes might be present.
                                                                                                                         ATTTTGTTGCCCCTTTAGTGCCATTCGGTTTGGGGATGGGACGTATCGGTAACTTTATGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCGGACTGTTTTTAGCTGGATACGGTACATTCCGCTTCCTTGTGGAATACGTCCGTGAGC
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   - TAATGGTGGCCCACTGCCGCGCCATCCTTCACAGCTTTATGAATTCGCCTTAGAAGGCG
                                     ACGCCGAGCTGTGGGGCAAACCCACCGACGTGCCATGGGCGATGATCTTCCCGCCGTTCA 134
                                                              ATAGTGAACTTTGGGGACGAGTAACGGATGTGCCTTGGGCCTTTTGTATTCCC------
                                                                                                   ATTTCGTTGCCCCGCTGGTGCCGATCGGCNTGGGTGCCGGGCGTATCGGCAACTTCATCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cytochromes and manganese oxidation in Pseudomonas
                                                                                                                                                                                                                                                                                                             /organism="Pseudomonas putida"
/mol_type="genomic DNA"
/strain="MnB1; ATCC 23483"
                                                                                                                                                                                                                                               /clone="transposon-tagged mutant UT502"
/clone_lib="Pseudomonas putida MnB1; ATCC
/note="manganese oxidizing bacterium"
                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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                                                                                                                                                                                                                                                                                               db_xref="taxon:303"
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                                                                                                                                                                 Score 115.6; DB 29;
Pred. No. 3.8e-22;
0; Mismatches 145;
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Matches 342
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: craymond Class: shotgun.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Whole-Genome-Sequence variation among multiple Psedomonas aeruginosa library J. Bacteriol. (2002) In press
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  University of Washington
Box 352145, Seattle, WA 98105-2145,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Spencer, D.H., Raymond, C.K., Smith, E.E., Burns, J.L., Kaul, R. and Olsen, M.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Chris K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pseudomonadaceae; Pseudomonas.
1 (bases 1 to 1034)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAGATGCTCAGTTGGG---TCTGTTTGGTGGCTTCATTTCAATGGGGCAAATCCTCTCCT
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                                                                                  TATGGCTTGATGTATTTGGTGGGTTTCCTTTTTGCTATGTGGTTGGCCAATCGCCGAGCG
AAGCGCTTCGACCCGACCTGGACCAAGGAGCGCCTTTCCGACCTGGTCTTCTGGGTTCGC
                            GATCGCGCGGCAGTGGTTGGACGCGTGAGCAAGTCTCTGACTTGTTATTC--
                                                             CTGACGTATCCCCAGATCGATCCGGTTGCGCTGGCCATCGGCCCGCTGAAGATCCACTGG
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                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 craymond@u.washington.
                                                                                                                                                                                                                                                                      /clone="pacs2-164_3389"
/clone lib="pacs2-164"
/note="clinical isolate 2-164 Whole
library."
                                                                                                                                                                                                                                                                                                                                                     /mol_type="genomic DNA"
/strain="2-164"
                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:287"
                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                     organism="Pseudomonas aeruginosa"
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PTWM04242 Phaeodactylum tricornutum Uni-Zap
tricornutum cDNA 5', mRNA sequence.
CD379073
                                                                                                                                                                                                                                      Laboratory of Molecular Plant Biology Stazione Zoologica 'Anton Dohrn' Villa Comunale, I-80121, Napoli, Ital Tel: 39 081 583 3268/3211
Fax: 39 081 764 1355
                                                                                                                                                                                                                                                                                                                                                                                                                   Phaeodactylum tricornutum
Phaeodactylum tricornutum
Elacillariophyta; Bacillariophyceae;
Bukaryota; stramenopiles; Bacillariophyta; Bacillariophyceae;
Bacillariophycidae; Naviculales; Phaeodactylaceae; Phaeodactylum.
1 (bases 1 to 878)
                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 878)
Scala,S., Carels,N., Falciatore,A., Chiusano,M.L. and Bow.
Genome properties of the diatom Phaeodactylum tricornutum
Plant Physiol. 129 (3), 993-1002 (2002)
                                                                                                                                                                          Seq primer
POLYA=Yes.
                                                                                                                                                                                                        Email: chris@alpha.szn.it
Diatom EST Database(http://avesthagen.sznbowler.com)
                                                                                                                                                                                                                                                                                                                       Contact: Bowler C
                                                                                                                                                                                                                                                                                                                                        12114555
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                                                                                                                                                                                        primer: T3 backward
                               ਨ
                                         /organism="Phaeodactylum tricornutum"

|mol_type="mRNA"

|db_xref="taxon:2850"

|cell_line="CCWP632"

|clone_lib="Phaeodactylum tricornutum Uni-Zap

|note="Vector: Uni-Zap XR vector; Site_1: Eco
                                                                                                                                         j. .878
                                                                                                                                                         Location/Qualifiers
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S 밁 Ś 밁

mRNA

Uni-Zap XR Phaeodactylum linear

EST 31-MAY-2003

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and Bowler, C. Phaeodactylum.

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SOURCE
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AUTHORS
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Best Local S
Matches 186
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                    Laboratory of Molecular Plant Biology
Stazione Zoologica 'Anton Dohrn'
Villa Comunale, I-80121, Napoli, Ital'
Tel: 39 081 583 3268/3211
Fax: 39 081 764 1355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases I to 921)
Scala, S., Carels, N., Falciatore, A., Chiusano, M.L. and Bowler, C.
Genome properties of the diatom Phaeodactylum tricornutum
Plant Physiol. 129 (3), 993-1002 (2002)
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                                                                                                                                                                                                                                                                                              Email: chris@alpha.szn.it
Diatom EST Database(http://avesthagen.sznbowler.com)
Seq primer: T3 backward
POLYA=Yes.
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Eukaryota; stramenopiles; Bacillariophyta; Bacillariophyceae;
Bacillariophycidae; Naviculales; Phaeodactylaceae; Phaeodacty
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CD382942.1 GI:31258556
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   ATCATTTCTAGAGGTAGGAAGATCAGCACCGCGAGAAGATTGAAAAAATCGTGGATGGTG
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                                                                                                                             /clone_lib="Phaeodactylum tricornutum Uni-Zap XR"
/note="Vector: Uni-Zap XR vector; Site_1: Eco RI; Site_2:
Xho I"
                                                                                                                                                                              /mol_type="mkNA"
/db_xref="taxon:2850"
/cell_line="CCMP632"
                                                                                                                                                                                                                      /organism="Phaeodactylum tricornutum"
/mol_type="mRNA"
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Pred. No. 1.2e-20;
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Genome properties of the diatom Phaeodactylum tricornutum
Plant Physiol. 129 (3), 993-1002 (2002)
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Phaeodactylum tricornutum
Phaeodactylum tricornutum
Eukaryota; stramenopiles; Bacillariophyta; Bacillariophyceae;
Bacillariophycidae; Naviculales; Phaeodactylaceae; Phaeodacty
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Diatom EST Database(http://avesthagen.sznbowler.com)
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                                                                                         ATCATTTCTAGAGGTAGGAAGATCAGCACCGCGAGAAGATTGAAAAAATCGTGGATGGTG
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                                                                                                                                                                                                                                                        /organism="Phaeodactylum t
/mol_type="mRNA"
/db_xref="taxon:2850"
/cell_line="CCMP632"
/clone_lib="Phaeodactylum
                                                                                                                                                                                                                    /cell_line="CCMP632"
/clone_lib="Phaeodactylum
/note="Vector: Uni-Zap XR
Xho I"
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                                                                                                                              Score 106.2; DB 14,
Pred. No. 3.1e-19;
D; Mismatches 128;
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tricornutum Uni-Zap
vector; Site_1: Eco

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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: zbrafish@watson.wustl.edu
Library materials provided by G. Elgar (UK MRC HGMP-RC) Library
constructed by Drs. K. Kawakami, M. Sasaki, S. Sugano, K. Kikuchi
and S. Watabe (University of Tokyo, Institute of Medical Science
and Laboratory of Aquatic Molecular Biology and Biotechnology) DNA
Sequencing by: Washington University Genome Sequencing Center Clone
distribution: Fugu clone distribution information can be found
through the LM.A.G.E. Consortium/LLNL, send email to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clark, M., Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M., Eddy, S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylle, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R.,
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei

Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;

Tetradontoidea; Tetraodontidae; Takifugu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Waterston, R. and Wilson, R. WashU Zebrafish EST Project 1998 Unpublished (1998) Contact: Stephen L. Johnson Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. I Tel: 314 286 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SYSTEM PROTEIN. ;, mRNA sequence. CA588286 CA588286.1 GI:25132864
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                           info@image.llnl.gov
Seq primer: T3 ET from Amersham
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                                                                                                                                                                                                                                                                                                                                                       quality sequence stop: 496.
Location/Qualifiers
/dev stage="adult"
/lab_host="DH10B (T1 phage-resistant)"
/clone lib="Fugu UT6 adult gut"
/note="Vector: pBluescript-FL; Site_1: PflM I
(CCANNNNNTGG); Site_2: PflM I (CCANNNNTGG); BamHI-SmaI
sites were converted to BamHI-PflMI-SfiI-PflMI sites (Sm
is destroyed). Other part of the vector is untouched. The
                                                                                                                                                                                                                     /mol_type="mRNA"
/db_xref="taxon:31033"
/clone="IMAGE:6351812"
                                                                                                                                                                                                                                                                                                     organism="Takifugu rubripes"
                                                                                                                                                                                              tissue_type="gut"
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CDNA is inserted between two PfIMI sites in T3 (5') to T7 (3') direction. Library materials provided by G. Elgar (UK MRC HGMP-RC) and constructed and donated by Drs. K. Kawakami, M. Sasaki, S. Sugano, K. Kikuchi and S. Watabe (University of Tokyo, Institute of Medical Science and Laboratory of Aquatic Molecular Biology and Biotechnology)."

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AUTHORS
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Best Local Similarity
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CE 1 (bases 1 to 813)

Clark, M., Johnson, S. L., Lehrach, H., Lee, R., Li, F., Marra, M., Eddy, S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.

Waterston, R. and Wilson, R.

WashU Zebrafish EST Project 1998

11 Unpublished (1998)
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Email: zbrafish@watson.wustl.edu
Library materials provided by G. Blgar (UK MRC HGMP-RC) Library
constructed by Drs. K. Kawakami, M. Sasaki, S. Sugano, K. Kikuchi
and S. Watabe (University of Tokyo, Institute of Medical Science
and Laboratory of Aquatic Molecular Biology and Biotechnology) DNA
Sequencing by: Washington University Genome Sequencing Center Clone
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                                                                                                                                                                              Contact: Stephen L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. 1
                                                                                                                                       Tel: 314 286 1800
Fax: 314 286 1810
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     TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      196;
                                                                                                                                                                                                                                                                    828 bp mRNA
AGENCOURT 10670196 NCI CGAP ZKidl Danio
IMAGE:6797422 5', mRNA sequence
CA475087
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                   Actinopterygii; Neopterygii; Tele Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 828)
                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Actinopterygii; Neopterygii; Teleostei;
                                                                                                                                                                                                                                    CA475083
CA475083.1 GI:24931435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       distribution: Fugu clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL, send email to:
                                                                                                                                                           Danio rerio
                                                                                                                                                                                    Danio rerio (zebrafish)
                                                                                                                                                                                                               EST
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Seq primer: T3 ET from Amersham
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//dev_stagg="adult"
//lab_host="pH10B (T1 phage-registant)"
//clone_lib="Fugu UT6 adult gut"
//clone_registed Sites if I pfiMI sites (SmaI sites were converted to BamHI-pfiMI sites in T3 (5') to T7
//clone_lib="fugu UT6 adult gut"
//clone_lib="f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biotechnology)."
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|mol_type="mRNA"
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Pred. No. 1.6e
0; Mismatches
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                             Satou, Y.,
Satoh, N.
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Tissue Procurement: Leonard I. Zon, M.D.

CDNA Library Preparation: Invitrogen Corp

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can
                                             Eukaryota; Metazoa; Chordata; Urochordata; Phlebobranchia; Cionidae; Ciona.

1 (bases 1 to 685)
Satou,Y., Satake,M., Azumi,K., Nonaka,M.,
                                                                                                                                                                                                               EST
                                                                                                                                                                                                                                                                                                               BW039803 Region Satch unpublished
                                                                                                                                                           Ciona intestinalis
                                                                                                                                                                                                                                    BW039803.1
                                                                                                                                                                                                                                                                  BW039803
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intestinalis cDNA clone cibd041k19 5', mRNA sequence.
вмолявла
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Location/Qualifiers
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  Expressed
                                                                                                                                                                                      Ciona intestinalis
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http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTGACGAGAGTATTGGTCACAGTAGTACCAATATTGGCACCCATCACCATAGGAATCGCG 2644
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/db_xref="taxon:7955"
/db_host="DH108 [71-resistant)"
/lab_host="DH108 [71-resistant)"
/clone = lib="MCI CGAP_ZKiddl"
/clone = lib="MCI CGAP_ZKiddl"
/note="organ: kidney; Vector: pCMV-SPORT6.1; Site_1:
/ECORV; Site_2: Not1; Cloned unidirectionally. Primer:
Oligo dT. Average insert size 1.8 kb. Constructed by J.
Wang (Research Genetics, Invitrogen Corp) from tissue
donated by L. Zon (Harvard University). Note: this is a
NCI_CGAP_Library."
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     genes in Ciona
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                                                                                                                                   Chordata; Urochordata; Ascidiacea;
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Pred. No. 2.4e-18;
0; Mismatches 119
     intestinalis (2002)
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RESULT 15
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                                 Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502,
Tel: 81-75-753-4081
Fax: 81-75-705-1113
                                                                                                                        Expressed genes in Ciona Unpublished (2002) Contact: Nori Satoh
                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Phlebobranchia; Cionidae; Ciona.

1 (bases 1 to 686)

1 (bases 1, Y., Satake, M., Azumi, K., Nonaka, M., Shin-i, T., Ko
                                                                                                                                                                                                                                                                  Ciona intestinalis
Ciona intestinalis
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                                                                                                       Contact: Nori Satoh
Department of Zoology
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Department of Zoology
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satoh@ascidian.zool.kyoto-u.ac.jp.
Location/Qualifiers
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